

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:52 ; Search time 53.5 Seconds
(without alignments)
901.621 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1863
Sequence: 1 MASLGLTALAAATLAPGA.....VELVAIVNPALSALSPDSIKM 362

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

Minimum number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
A.Geneseq_101002.*
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	16 AAM00635	ILTV glycoprotein
2	1863	100.0	362	17 AAM06787	ILTV glycoprotein
3	156	8.4	384	15 AAR47236	Wild-type feline H
4	152	8.2	355	18 AAM13105	Marek's disease vi
5	152	8.2	355	18 AAM11475	Marek's disease vi
6	148	7.9	364	18 AAM22999	Canine herpesvirus
7	148	7.9	364	19 AAM72659	Canine herpes viru
8	148	7.7	364	22 AAB51316	Pseudorabies virus
9	143.5	7.7	350	8 AAP0645	Glycoprotein 63 (g
10	143.5	7.7	350	15 AAR63143	

11	143.5	7.7	350	22 AAE0396	Pseudorabies virus
12	143	7.7	317	16 AAR80637	Bovine herpes viru
13	142.5	7.6	350	22 AAD04970	Pseudorabies virus
14	141.5	7.6	350	22 AAB82502	Pseudorabies virus
15	140.5	7.5	380	15 AAR48063	Sequence of polye
16	138	7.5	371	22 AAB78825	Pseudorabies virus
17	138	7.4	370	21 AAY32474	DNA encoding feli
18	135	6.7	356	17 AAM03136	Herpesvirus of tur
19	125	6.7	356	17 AAM03323	Herpesvirus of tur
20	123.5	6.6	356	17 AAR23323	Herpesvirus of tur
21	114	6.1	456	14 AAR33160	Human secreted pro
22	112	6.0	387	20 AAY08621	Human secreted pro
23	112	6.0	387	21 AAY06312	Human secreted pro
24	109.5	5.9	454	14 AAR33181	Human secreted pro
25	108.5	5.8	319	22 AAB65348	Human secreted pro
26	108	5.8	319	22 AAB85878	Human secreted pro
27	107	5.7	372	16 AAR52164	Human secreted pro
28	107	5.7	433	19 AAW72144	Human secreted pro
29	107	5.7	433	19 AAW72012	Human secreted pro
30	105.5	5.7	378	22 AAM39027	Human secreted pro
31	103	5.5	982	22 AAB58158	Human secreted pro
32	102.5	5.5	379	20 AAY25768	Human secreted pro
33	102.5	5.5	4498	22 AAB58595	Human secreted pro
34	102	5.5	234	12 AAB33907	Human secreted pro
35	98	5.3	503	12 AAR14768	Human secreted pro
36	97.5	5.2	1714	23 AAB60186	Human secreted pro
37	96	5.2	1296	23 AAB66702	Human secreted pro
38	96	5.2	1296	23 AAB66756	Human secreted pro
39	95	5.1	745	22 AAB71016	Human secreted pro
40	94.5	5.1	307	19 AAM38334	Human secreted pro
41	94	5.1	886	22 AAB64308	Human secreted pro
42	93.5	5.0	907	16 AAP50073	Human secreted pro
43	93.5	5.0	907	16 AAR80144	Human secreted pro
44	93.5	5.0	907	21 AAY68009	Human secreted pro
45	93	5.0	320	22 AAG91867	Human secreted pro

ALIGNMENTS

RESULT 1	AAW0635	standard; Protein: 362 AA.
ID	AAW0635	standard; Protein: 362 AA.
AC	AAW0635;	
XX		
DT	19-NOV-1996	(first entry)
XX		
DE	ILTV glycoprotein gl.	
XX		
KV	Infectious laryngotracheitis virus; ILTV; herpesvirus;	
KV	attenuation; vector: vaccine; chicken; poultry; immunisation;	
KV	glycoprotein gl.	
XX		
OS	Infectious laryngotracheitis virus.	
XX		
PN	MO9508622-AL.	
XX		
PD	30-MAR-1995.	
XX		
PF	16-SEP-1994.	94MO-US10628.
XX		
PR	24-SEP-1993.	93US-0126597.
XX		
PA	(SYTR) SYNTRO CORP.	
XX		
PT	Cochran MD, Wild MA:	
XX		
DR	WPI: 1995-139591/18.	
XX		
PT	N-PSDB: AAT33504.	
XX		
PT	Recombinant attenuated infectious laryngotracheitis virus - for use	
	in vaccines to protect poultry from infection from the virus, also	

PT methods of distinguishing between vaccinated and naturally infected
birds

Example 1: Page 102-103; 177pp; English.

CC The gi gene, spanning nucleotides 9874-10962 of the unique short
CC region (AAT33504) of infectious laryngotracheitis virus (ILT),
CC codes for a glycoprotein (AAM06787) of approx. 39,753 mol.wt.
CC The gi glycoprotein is homologous to Varicella-zoster gi.
CC Deletion of the gi gene results in an attenuated ILTV that
CC is useful as a vaccine against ILT disease in chickens.
CC Recombinant virus deleted for gi was safe in animal trials.
CC Deletion of the gi gene serves as a negative marker to
CC distinguish vaccines from infected animals. A gene coding
CC for a foreign antigen may be inserted into the gi gene to
CC produce a recombinant multivalent vaccine.

Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 16; Length 362;

Best Local Similarity 100.0%; Pred. No. 3.7e-174;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATIQLQLEFMPGQ 60
QY 1 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 121 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 121 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 181 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 181 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 241 WLENGVDHIEPTPANENSVTVRLGTMSPTLIGVYAAVVSATIGLVYISIVTRMCTP 300
DB 241 WLENGVDHIEPTPANENSVTVRLGTMSPTLIGVYAAVVSATIGLVYISIVTRMCTP 300
QY 301 HKRLDVSODDERSGTRESKRFSGPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HKRLDVSODDERSGTRESKRFSGPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 2

AAM06787

ID AAM06787 standard; Protein; 362 AA.

AC AAM06787;

DT 02-JUN-1997 (first entry)

DE ILTV glycoprotein gi.

KM ILTV; vaccine; vector; attenuation; poultry;

KM avian infectious bronchitis virus; Newcastle disease virus;

KM infectious bursal disease virus of chickens;

KM Marek's disease virus; herpesvirus; glycoprotein gi.

OS Infectious laryngotracheitis virus USDA strain 8302.

XX Key Location/Qualifiers

XX Peptide 1..22

XX Protein /label= Sig-peptide 23..362

FT Region /label= Mat_protein
FT 272..292
FT /label= Transmembrane_helix

PN W09629396-A1.

PD 26-SEP-1996.

PF 21-MAR-1996; 96WO-US03916.

PR 06-JUN-1995; 95US-0468190.

PR 23-MAR-1995; 95US-0410121.

XX (SYTR) SYNTRO CORP.

XX Cochran MD, Wild MA;

XX MPI: 1996-443172/44.

XX N-PSDB; AAT44384;

XX N-PSDB; AAT44385.

PT Recombinant infectious laryngotracheitis virus with deletion in the

PT glycoprotein G, gi or US2 gene, etc. - useful for vaccines against

PT infectious laryngotracheitis in poultry

XX Example 11: Page 110-111; 216pp; English.

CC Glycoprotein gi (AAM06787) is encoded by ORF8 of the unique short
CC region (AAT44384) of infectious laryngotracheitis virus (ILT). It
CC shows homology to the Varicella zoster virus gi glycoprotein.
CC Recombinant ILTV gi protein produced in a swinepox virus reacts to
CC convalescent sera from ILTV-infected chickens. Deletion of the gi
CC gene results in an attenuated ILTV that is useful as a vaccine and
CC as a negative marker to distinguish vaccinated from infected
CC animals. Insertion of a foreign gene into the gi gene allows
CC prodn. of multivalent vaccines.

Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 17; Length 362;

Best Local Similarity 100.0%; Pred. No. 3.7e-174;

Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATIQLQLEFMPGQ 60
DB 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATIQLQLEFMPGQ 60
QY 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 121 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 121 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 181 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
DB 181 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCSTRSSSVFVGCVTEYTFSSNRLTG 120
QY 241 WLENGVDHIEPTPANENSVTVRLGTMSPTLIGVYAAVVSATIGLVYISIVTRMCTP 300
DB 241 WLENGVDHIEPTPANENSVTVRLGTMSPTLIGVYAAVVSATIGLVYISIVTRMCTP 300
QY 301 HKRLDVSODDERSGTRESKRFSGPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HKRLDVSODDERSGTRESKRFSGPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 3

AA047236
ID AA047236 standard; Protein: 384 AA.
XX
AC AA047236;
XX
DT 06-SEP-1994 (first entry)
XX
DE Wild-type Feline Herpes Virus ORF-1-encoded protein.
XX
DE Feline herpes virus; FHV; genome; mutant; vaccine; ORF-1;
XX
KM Feline viral rhinotracheitis; herpesviridae family;
XX
KM herpes virus A subfamily.
XX
OS Feline Herpes Virus.
XX
PN MO9403621-A.
XX
PD 17-FEB-1994.
XX
PD 23-JUL-1993; 93MO-EP01971.
XX
PR 30-JUL-1992; 92EP-0202365.
XX
PA (ALKU) AKZO NV.
XX
PI Sondermeijer PJA, Willemse MJ;
XX
DR WPI: 1994-065709/08.
XX
DR N-PSDB: AA056188.
XX
PT Feline herpes virus mutant comprising a heterologous gene
XX
PT inserted in the virus genome - for vaccination against feline
XX
PT herpes virus and other feline pathogens.
XX
PS Claim 2; page 37-38; 55pp; English.
XX
CC Mutant versions of the wild-type feline herpes virus genome (AA056188)
XX
CC are claimed. Esp. the FHV mutant is one which fails to produce one
XX
CC or more antigenic or functional polypeptides. The mutant may contain
XX
CC a heterologous nucleic acid sequence inserted within one of the 6
XX
CC open reading frames. The attenuated FHV mutants can be used to prepare
XX
CC vaccines against feline viral rhinotracheitis and, where the
XX
CC heterologous insert encodes an antigen of a feline pathogen,
XX
CC against other infectious diseases of felidae.
XX
SQ Sequence 384 AA;
XX
Query Match 8.4%; Score 156; DB 15; Length 384;
Best Local Similarity 23.3%; Pred. No. 1.6e-06;
Matches 75; Conservative 48; Mismatches 141; Indels 58; Gaps 12;
DB 5 LGTLLALATLAPGAMGIVITGNHVSARIDDDHIVAPRPE-ATIQLOLFMPGO-RP 62
DB 1 MSTATIYILMAIGTVIGIVRGDHSLVHDTSSGFVITPLENTIYGLHILDDQPLP 60
DB 63 HKRYSGTVAVAFRSDITNOCYOELSEERFENCTHRSSVFGC--KTEYTFESNRRLG 120
DB 61 VNNINGTLEI-ITHNHSSCYKIVQVETSSCFVRNNRNFSCLAHKSMDQIDOLISINTS 119
DB 121 PPHFKITIRNRPNDSCMEYVIVRLDDTKEPIDVFAIQLSYQFANTATRGLYSKASC 180
DB 120 VETGMLITTSRPMEDGGIYALRVRFNNNRK-ADVFGSLVFYSP---DTRGHRHAD- 173
DB 181 RTGGLPVQLEAVYLRTESSMRNQAVYATVATTSSEATPTPVATASASLEAEHFTFP 240
DB 174 -----ENNGEILITPS--SMETVYKVTPIYDHMVTQ---ISNKSMSSE---P 216
DB 241 WLENGVDHYEPTPANDNSNVTVR-----GTMSPTLLGVVAVAVVSAT- 283
DB 217 SNTSISCHTFQNDPNFEGELVYTHLNLINAGNITYDDVMGDTTLAGRLIDKMLNLSYSSP 276
DB 284 -----IGLVIVISI 292
: | | | | |

DB 277 KNETTOKWTPDRKGVIVISI 298
RESULT 4
ID AA013105
XX
AC AA013105 standard; Protein: 355 AA.
XX
DT 12-MAY-1997 (first entry)
XX
DE Marek's disease virus type 1 glycoprotein I.
XX
DE GA strain; glycoprotein; gp1; gp2; recombinant virus;
XX
KM Newcastle disease virus; herpes virus; vaccine.
XX
OS Marek's disease virus type 1.
XX
PN JP09009978-A.
XX
PD 14-JAN-1997.
XX
PD 26-APR-1996; 96JP-0131084.
XX
PR 28-APR-1995; 95JP-0129523.
XX
PA (JAPC) JAPANESE GEON CO LTD.
XX
DR WPI: 1997-126432/12.
XX
DR N-PSDB: AAT61883.
XX
PT Recombinant virus contg. herpes virus glyco:protein gp1 - and
XX
PT effective Newcastle disease vaccine contg. it
XX
PS Claim 5; Pages 14-15; 20pp; Japanese.
XX
CC The present sequence encodes the Marek's disease virus (MDV) type 1
XX
CC (GA strain) glycoprotein (gp1). A recombinant virus containing the
XX
CC gene encoding MDV gp2, and optionally also gp1, in a genomic region
XX
CC unessential for its growth, can be used as the effective component
XX
CC in a Newcastle disease virus vaccine.
XX
SQ Sequence 355 AA;
XX
Query Match 8.2%; Score 152; DB 18; Length 355;
Best Local Similarity 22.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;
DB 19 GAMGIYITGNHVSARIDDDHIVAPRPE-ATIQLOLFMPGOGRHKRYSGTVAVAFRSD 77
DB 15 GIMSIYITGTSVLTSTDSALVAFCGLDKKVNVNRGLFLDDQRTSSYGTLEI-LKWD 73
DB 78 ITNOCYOELSEERFENCTHRSSVFGCKTEYTESASNRLLGPPHFK--LTIRNRP 134
DB 74 EEYKCYSLVHATSYMDCPAIDATVFRGCRDVAVYVAPDHRV--OPFEKGTLLRIVEPRV 131
DB 135 NDGMPYVIVRLDDTKEPIDVFAIQLSYQFANTATRGLYSKASCRTFGLPVQLEAVL 194
DB 132 SDGSGYIIVALAG-RNMSDIFRMAVIRIS-----SKSWACNHSASFQAHKCI 179
DB 195 RTEE--SMRNMQAVYATVATTSSEATPTPVATASASLEAEHFTPMLNCGVDHYEPT 252
DB 180 RYVDRAFERNYLIGHVGLDSDSELAITNIPGIS-TQINITTPFDNNGSTIYSP 238
DB 253 P---ANENSVYVRIGT-MSPTLLGVVAVV--SATIGLVIV--ISITRNMCPTPHK 303
DB 239 VFNLFNNSHVNDAMNSGMMNTVILKYLPLRILFISFMIVLCIALIATIVICBGRBPHRR 298
DB 304 LDTVQDDDERSGQTRRESKRGFPVACEIRKGDQDSELYE 344
DB 299 I---YIGERDSE-----APLITSAVNESFOYIYNKE 328
: | | | | |

```

RESULT 5
AAW11475
ID AAW11475 standard; Protein: 355 AA.
XX
AC AAW11475;
XX
DT 30-APR-1997 (first entry)
XX
DE Marek's disease virus glycoprotein gI.
XX
KM MDV; UL32; membrane glycoprotein 82; glycoprotein gI; antigen;
XX vaccine; vector; fowlpox virus.
XX
OS Marek's disease gammaherpesvirus type 1 strain GA.
XX
PN W09703187-A2.
XX
PD 30-JAN-1997.
XX
PF 05-JUL-1996; 96WO-US11360.
XX
07-JUL-1995; 95US-0499474.
XX
PA (JAPG ) NIPPON ZEON KK.
XX (USDA ) US SEC OF AGRIC.
XX
PI Lee LF, Nazerian K, Witter RL, Wu P, Yanagida N;
XX Yoshida S;
XX
DR WPI; 1997-119044/11.
XX
PT New DNA encoding glycoprotein 82 of Marek disease virus - useful in
XX vaccines to protect poultry
XX
PS Disclosure; Page 72-73; 101pp; English.
XX
CC Genes encoding Marek's disease virus glycoprotein gI (AAW11475)
XX and/or glycoprotein gE (AAW11474) can be incorporated into
XX recombinant viral vectors that also carry the UL32 gene (see also
XX AAT51358) encoding glycoprotein 82 (AAW11473). The gI and gE genes
XX were cloned from MDV genomic DNA by PCR (see also AAT51366-69 and
XX AAT51366-67). A transfer vector was constructed that was used to
XX produce a recombinant fowlpox virus useful as a vaccine to
XX protect poultry against MDV infection.
XX
SQ Sequence 355 AA:
XX
Query Match 8.2%; Score 152; DB 18; Length 355;
Best Local Similarity 22.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;
XX
19 GAWGIVITGNHVSARIDDDHIVYAPRPE-ATIQQLFFMPCGRPHKPYSGTVRVAFRSD 77
15 GIMSIYVTGVSATLSTDSALVAFGLDKMNVNRGLLFLGDTTRSSVTGTEI-LKMD 73
XX
78 ITNOCQELSEEFENCNHRSSVFCVTEYTESASNRRLGPPHPEK---LTINPRP 134
74 EEKCKSVLHATSYMCCPAIDATVEFRCDAVVAQPHDRV--QPPPEKGTLLRIYEPHY 131
XX
135 NDSGMFYVVRIDDTKEPIDVFAIOLSVQFANTATRGLYSASRTGGLPYOLEAVL 194
132 SDTGSTYITVALAG-RNMSDIFRMAVIRNS-----SKSMACHNSASSFOAHKCI 179
XX
195 RTEE--SMRNMOAYVATEATTSAEATPTPVATASASELEAHFTFPLENGVDHYEPT 252
180 RYVDRAAFENYLIGHGNLSDSELMHAIYINITPOS--TDINIITPPYDNGTITSPT 238
XX
253 P---ANENSNTVVRIGT--MSPTLIGTVAAV--SATIGLVIV---ISIVTRNMTCPARK 303
239 VFNLFNNSHVDAMNSTMGMNTVLKTYLPRLIYFTMIYICIAIALIYLCERCSPHRR 298
XX
304 LDTVSDDEBSQTRRESRRKFGPMVACEINKGADDSOLVE 344
XX

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DB 299 I-----YIGEPKRSDE-----APLITSAVNESFOYDYNKE 328
RESULT 6
AAW22999
ID AAW22999 standard; Protein: 364 AA.
XX
AC AAW22999;
XX
DT 20-FEB-1998 (first entry)
XX
DE Canine herpesvirus glycoprotein I PCg1364.
XX
KM Vaccine; vector; gene therapy; canid; dog; CHV; CgI; PCg1364;
XX glycoprotein I.
XX
OS Canine herpesvirus.
XX
PN W09729772-A1.
XX
PD 21-AUG-1997.
XX
PF 14-FEB-1997; 97WO-US04115.
XX
PR 15-FEB-1996; 96US-0602010.
XX
XX (HESK-) HESKA CORP.
XX
PI Frank RA, Haanes EJ;
XX
DR WPI; 1997-424758/39.
XX
DR N-PSDB; AAT75616.
XX
PT Recombinant canine herpes virus and its genome - useful as vaccine
XX to protect canids against infectious, metabolic or genetic diseases
XX
PS Claim 57; Page 181-182; 240pp; English.
XX
CC This protein comprises canine herpesvirus (CHV) glycoprotein I
XX (PCg1364). Its sequence was deduced from a coding region found in
XX CHV genomic DNA molecule ncus10592 (see AAT75616). PCg1364 can be
XX expressed in transformed host cells. CHV proteins, nucleic acids,
XX and antibodies raised against CHV proteins, can be used to protect
XX canids against CHV infection. Novel recombinant CHV and novel
XX recombinant CHV genomes that contain heterologous nucleic acid
XX molecules inserted e.g. into CgI gene, can be used as vaccines to
XX protect canids against infectious, metabolic or genetic diseases.
XX
SQ Sequence 364 AA:
XX
Query Match 7.9%; Score 148; DB 18; Length 364;
Best Local Similarity 27.3%; Pred. No. 8.9e-06;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
XX
4 LGLTALLAATAPRGMAMIVITGNHVSARIDDDHIVYAPRPEATIQQLFFMPCGR-P 62
16 LITMPLPLFLFLYGVNGVFYKGYISMFLMTSSGFSIFPPDKFLVSGRLFLDDOHL 75
XX
63 HKPVSQTVAVAFRSDITNOCYOELSEEFENCNHRSSVFCG--KVTEYTESASNRRLG 120
76 VNNYSCTIEFT---HFNNSCTIVYQOTIEYFSCPRIFNNMFRSGCLKVSNHHSQLRINS 132
XX
121 PPHPEKLTIRNPRPNDSGMFYIVRLDDTKEPIDVFAIOLSVYQF 165
133 IENGVLLETINPKPNDSGVYFIRVOLENKK--TDVGIGIAFIYSF 175
XX
RESULT 7
AAW72659
ID AAW72659 standard; Protein: 364 AA.
XX
AC AAW72659;
XX

```


DT 07-JAN-1999 (first entry)
 XX Canine herpes virus protein sequence P0GI-364.
 DE
 XX
 XX Canine herpes virus; CHV; recombinant canine herpes virus vector.
 KW genome; vaccination; dog; protozoan; helminth; ectoparasite; bacteria;
 JW virus infection.
 XX
 OS Canine herpes virus.
 XX
 PN US5804197-A.
 XX
 PD 08-SEP-1998.
 XX
 PF 12-JUL-1996; 96US-0680726.
 XX
 PR 12-JUL-1996; 96US-0680726.
 PR 15-FEB-1996; 96US-0602010.
 PR (HESK-) HESKA CORP.
 PI Frank RS, Haanes EJ;
 XX WPI; 1998-505590/43.
 DR N-PSDB; AAV6941.
 XX
 XX Canine herpes virus nucleic acids - useful for producing recombinant
 PT canine herpes virus vectors
 PS Claim 7; Column 133-136; 103pp; English.
 CC The present sequence represents a canine herpes virus (CHV) protein
 CC sequence. The nucleic acid sequence which encodes the protein can be
 CC used for DNA vaccination of dogs against CHV and also other infective
 CC agents such as protozoans, helminths, ectoparasites, bacteria and
 CC viruses. CHV can be formulated by incorporation of heterologous nucleic
 CC acid molecules as a single multivalent therapeutic composition against
 CC a variety of canine pathogens.
 CC
 XX
 SO Sequence 364 AA;
 Query Match 7.9%; Score 148; DB 19; Length 364;
 Best Local Similarity 27.3%; Pred. No. 8.9e-06;
 Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
 4 LGCTIALAATLAPGANGIVITGNHVSARIDDDHIVAPPEATTQLOLFMPGQR-P 62
 16 LLITMFLPIFLFYGVNGFYKGTYSMFLNTSSGFSIFPDKFIYSGRLFLDDQHL 75
 63 HKPYSGTVARAFRSDITNOCYQELSEERFNCNTHRSSSVFVGC--KVTEYTFASNRLTG 120
 76 VNNISGTFIEFT--HNNSCTVYQTEYFSCPRIFNNAFRCLKVKSKHHEGQLINSS 132
 121 PPHPEKLTINRPNDGMEFYVIRLDDTEPEIDVAIOLSYQF 165
 133 IENGVLLEITNRPNDGCVYFIKVLQLENNK--TDVGIFAFYISF 175
 DB
 RESULT 8
 ID AAB51316
 XX AAB51316 standard; Protein: 364 AA.
 AC
 XX AAB51316;
 XX
 DT 29-MAR-2001 (first entry)
 XX
 XX Canine herpes virus protein sequence SPQ ID NO:56.
 DE
 XX
 XX Canine herpes virus; CHV; antiallergic; immunosuppressive; cytostatic;
 KW antibacterial; antiinflammatory; vaccine; candid; infectious disease;
 KW genetic disease; metabolic disease; abnormal; cell growth; allergy;
 KW degenerative process; immunological defect; autoimmune disease; cancer;
 KW cardiovascular disease; graft rejection; haematopoietic disorder;

KW immunodeficiency disease; immunoproliferative disease; septic shock;
 KW immunosuppressive disorder; inflammatory disease; jaundice.
 XX
 XX Canine herpes virus.
 XX
 XX US6159478-A.
 XX
 PD 12-DEC-2000.
 XX
 PF 29-JAN-1998; 98US-0092409.
 XX
 PR 12-JUL-1996; 96US-0680726.
 PR 15-FEB-1996; 96US-0602010.
 PR (HESK-) HESKA CORP.
 PI Frank RS, Haanes EJ;
 XX WPI; 2001-090270/10.
 DR N-PSDB; AAF26761.
 XX
 XX Novel recombinant canine herpes virus protein useful for protecting
 PT animals, in particular candid from herpes virus infection and various
 PT diseases including cancer and autoimmune diseases
 XX
 XX Example 10; Column 135-136; 101pp; English.
 CC The present invention describes an isolated canine herpes virus (CHV)
 CC (I) CduPase protein encoded by a CHV nucleic acid molecule that
 CC hybridises under stringent hybridisation conditions with the CduPase
 CC gene. Also described is a therapeutic composition (II) comprising (I).
 CC (I) has antiallergic, immunosuppressive, cytostatic, antibacterial and
 CC antiinflammatory activities, and can be used in vaccines. (I) is useful
 CC for protecting an animal. In particular a candid from CHV. Therapeutic
 CC compositions comprising (I) are useful for treating infectious diseases,
 CC genetic diseases and other metabolic diseases, including diseases that
 CC lead to abnormal cell growth, degenerative processes and/or
 CC immunological defects, including allergies, autoimmune diseases,
 CC immunodeficiency diseases, graft rejection, haematopoietic
 CC disorders, cardiovascular diseases, cancer, immunoproliferative diseases,
 CC immunosuppressive disorders, inflammatory diseases, jaundice, and septic
 CC shock. CHV need not be attenuated for use as a live vaccine vector due
 CC to the low pathogenicity of maternal CHV, particularly as compared to
 CC that of other herpesviruses. AAF26720 to AAF26786 and AAB51303 to
 CC AAB51327 represent CHV nucleotides, proteins and PCR primers used in the
 CC exemplification of the present invention.
 CC
 XX
 SO Sequence 364 AA;
 Query Match 7.9%; Score 148; DB 22; Length 364;
 Best Local Similarity 27.3%; Pred. No. 8.9e-06;
 Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
 4 LGCTIALAATLAPGANGIVITGNHVSARIDDDHIVAPPEATTQLOLFMPGQR-P 62
 16 LLITMFLPIFLFYGVNGFYKGTYSMFLNTSSGFSIFPDKFIYSGRLFLDDQHL 75
 63 HKPYSGTVARAFRSDITNOCYQELSEERFNCNTHRSSSVFVGC--KVTEYTFASNRLTG 120
 76 VNNISGTFIEFT--HNNSCTVYQTEYFSCPRIFNNAFRCLKVKSKHHEGQLINSS 132
 121 PPHPEKLTINRPNDGMEFYVIRLDDTEPEIDVAIOLSYQF 165
 133 IENGVLLEITNRPNDGCVYFIKVLQLENNK--TDVGIFAFYISF 175
 DB
 RESULT 9
 ID AAF70645
 XX AAF70645 standard; Protein: 350 AA.
 AC
 XX AAF70645;
 XX
 DT 29-APR-1991 (first entry)

```

XX  Pseudorabies virus gp63 protein.
DE
XX  PRV; vaccine; GI: gp50; gp63.
XX
XX  Pseudorabies virus.
OS
XX  W08702058-A.
PN
XX  09-APR-1987.
PD
XX  28-AUG-1986; 86MO-US01761.
PE
XX  16-JUL-1986; 86US-0886260.
PR  04-OCT-1985; 85US-0784787.
PR  26-NOV-1985; 85US-0801799.
PR  26-MAR-1986; 86US-0844113.
PR  26-MAR-1986; 86US-0844133.
XX
XX  (UPJO ) UPJOHN CO.
PA  (PETR/) PETROVSKIS E. A.

XX  Petrovskis EA, Post LE, Timmins JG;
DR  WPI; 1987-108689/15.
DR  N-PSDB; AAN70994.
XX
XX  Pseudo-rabies virus protein - produced from recombinant DNA and
PT  used to produce vaccine and detect animals infected with virulent
XX  virus.
XX
XX  Claim 8; Page 59; 67pp; English.
XX
XX  The PRV glycoprotein product may be used as in vaccination of
CC  animals such as swine, sheep and goats against infection by the
CC  virus. The protein may be produced from a transformed expression
CC  system such as E.coli, yeast or CHO cells operatively linked to a
CC  suitable expression control sequence. Glycoproteins gp1 and gp63 may
CC  be used to distinguish between infected and vaccinated animals.
CC  See also AAN70993-5.
XX
XX
SQ  Sequence 350 AA:

Query Match 7.7%; Score 143.5; DB 8; Length 350;
Best Local Similarity 22.8%; Pred. No. 2.3e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

QY 8 LALLAATLAPFGAM--GIYITGNHVSARIDDDHIVARPREATIQLOLFPMGQRPKRP 65
   15 LLLAALTLLALTPRVGCVLEFRGAGSVNHVAGSAVLVPGDAPNLTIDGTLFLEGPSPSN- 73
QY 66 YSGTVAVAFRSIDITNOCYELSEERFENCTHRSSVFGC--KVTEYTFAS-----NRL 118
   74 YSGRVEL-LRLDPKRCACYTEVIAEYDLCPRVHNEAFRCGLRREPLARASAAVEARRL 132
DB 119 TGRPHFEKLTIRNPRDSGMFYIVRLDTPKRPIDVFAQLSVYOFANPAATRGV 174
   133 -----LFSVRPAPRDAGSYLVRAVNGT---TDLFVLTALV-----PRGRPHNR 174
QY 175 --YSKASCRFTGLPTVQLEAYLRTESWRNMQAYV--ATEATTSA-----EATPTPV 224
   175 TPSSADECR---PVV-----GSMHDSLAVVDPAEDAVFTTPPTPIRDEPTTPAPR 221
DB 222 RGTGATPEPRSDDEEDE-----EGATTAMTPVPGTLDANGTM--VLNASVSVLL 271
QY 225 TATSAS-----ELEAEHFTFPMLENGVDHYEPTPANENSNTVRLGMSPTLIGTV 277
   225 TATSAS-----LVYISITVRMCTPRHKLDTLVSDDDERSOTRRESRK 323
DB 272 AANMATAGARGPKIAMVLGPTIVLLIFLGVAACAARCAARGIASTGRDPGAARRSTR 331

```

```

AAR63143
ID  AAR63143 standard; Protein; 350 AA.
XX
XX  AAR63143;
AC
XX  12-JUN-1995 (first entry)
DT
XX  glycoprotein 63 (gp63) of pseudorabies virus.
DE
XX
XX  pseudorabies virus; PRV; glycoprotein; gp50; GI: gp63;
XX  determination; detection; vaccine; infected animal; isolation;
XX  cloning; virulence.
XX
XX  Pseudorabies virus.
OS
XX  US5352575-A.
PN
XX  04-OCT-1994.
PD
XX  04-OCT-1985; 85US-0784787.
PE
XX  04-OCT-1985; 85US-0784787.
PR  04-OCT-1985; 85US-0784787.
PR  26-NOV-1985; 85US-0801799.
PR  26-MAR-1986; 86US-0844113.
PR  16-JUL-1986; 86US-0886260.
PR  29-JUN-1987; 87US-0100817.
PR  20-APR-1990; 90US-0513282.
XX
XX  (UPJO ) UPJOHN CO.
PA
XX  Petrovskis EA, Post LE, Timmins JG;
XX
XX  WPI; 1994-316176/39.
DR  N-PSDB; AAO73489.
XX
XX  Identifying animals vaccinated against pseudorabies virus - by
PT  detecting the absence of GI or GP.63 antibodies in serum to
PT  distinguish vaccinated from infected animals
XX
XX
XX  Example 3; Column 21-24; 21pp; English.
XX
XX  AAR63143 shows the protein sequence of gp63 (glycoprotein) encoded by
CC  AAO73489, isolated from Pseudorabies virus (PRV). The DNA and protein
CC  sequences of the invention are useful in a method for distinguishing an
CC  animal vaccinated with a PRV vaccine lacking glycoprotein GI, GP63 or
CC  GP50 from an animal infected with a virulent wild-type PRV without
CC  sacrificing the animal. The method is used to test animals such as
CC  swine, cattle, sheep and goats. (see AAR63142 and AAR63144).
XX
XX
SQ  Sequence 350 AA:

Query Match 7.7%; Score 143.5; DB 15; Length 350;
Best Local Similarity 22.8%; Pred. No. 2.3e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

QY 8 LALLAATLAPFGAM--GIYITGNHVSARIDDDHIVARPREATIQLOLFPMGQRPKRP 65
   15 LLLAALTLLALTPRVGCVLEFRGAGSVNHVAGSAVLVPGDAPNLTIDGTLFLEGPSPSN- 73
DB 119 TGRPHFEKLTIRNPRDSGMFYIVRLDTPKRPIDVFAQLSVYOFANPAATRGV 174
   133 -----LFSVRPAPRDAGSYLVRAVNGT---TDLFVLTALV-----PRGRPHNR 174
QY 175 --YSKASCRFTGLPTVQLEAYLRTESWRNMQAYV--ATEATTSA-----EATPTPV 224
   175 TPSSADECR---PVV-----GSMHDSLAVVDPAEDAVFTTPPTPIRDEPTTPAPR 221
DB 222 RGTGATPEPRSDDEEDE-----EGATTAMTPVPGTLDANGTM--VLNASVSVLL 271
QY 225 TATSAS-----ELEAEHFTFPMLENGVDHYEPTPANENSNTVRLGMSPTLIGTV 277
   225 TATSAS-----LVYISITVRMCTPRHKLDTLVSDDDERSOTRRESRK 323
DB 272 AANMATAGARGPKIAMVLGPTIVLLIFLGVAACAARCAARGIASTGRDPGAARRSTR 331

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Db	272	RGTGATPPPRDEEDEE-----EGATTAMPVPGTLDANGTM---VLNASVSRLV	271
Oy	278	AVASATIG-----LVIVISITRMCIPPHKIDYTSODDERQSOTRESRK	323
Db	272	AAMATGACARGPKIAMTGPIVVLLIFLGACARCARCAGIASRGDPCAAARSSTR	331
RESULT 11			
ID	AAE05396		
XX	AAE05396 standard; Protein; 350 AA.		
XX	AAE05396;		
XX	24-SEP-2001 (first entry)		
XX	Pseudorabies virus (PRV) glycoprotein gp63.		
XX	Pseudorabies virus; PRV; glycoprotein; gp63; immunostimulant; vaccine;		
XX	PRV infection.		
XX	Pseudorabies virus.		
XX	Key Location/Qualifiers		
PH	Misc-difference 131	/note= "Encoded by GGG"	
FT	Misc-difference 132	/note= "Encoded by GTG"	
FT	Misc-difference 134	/note= "Encoded by CCG"	
FT	Misc-difference 144	/note= "Encoded by CCG"	
FT	Misc-difference 207	/note= "Encoded by CGG"	
FT	Misc-difference 222	/note= "Encoded by GGG"	
FT	Misc-difference 223	/note= "Encoded by CCG"	
FT	Misc-difference 284	/note= "Encoded by CCG"	
FT	Misc-difference 334	/note= "Encoded by GGC"	
PN	USG261563-B1.		
XX	17-JUL-2001.		
XX	07-JUN-1995; 95US-0485287.		
XX	20-APR-1990; 90US-0513282.		
XX	21-JUN-1994; 94US-0262813.		
XX	28-AUG-1986; 86MO-USO1761.		
XX	26-NOV-1985; 85US-0801799.		
XX	26-MAR-1986; 86US-0844113.		
XX	16-JUL-1986; 86US-0886260.		
XX	29-JUN-1987; 87US-0100817.		
PA	(PHMA) PHARMACIA & UPJOHN CO.		
XX	Petrovskis EA, Post LE, Timmins JG;		
XX	WPI: 2001-450478/48.		
DR	N-PsDB; AAD10195.		
PT	Polypeptide comprising a pure and isolated pseudorabies virus gp63		
CC	polipeptide or its fragments, useful as a vaccine for protecting		
CC	animals against pseudorabies virus infection -		
PS	Claim 1: Column 39-40; 21pp: English.		
XX	The invention relates to pseudorabies virus (PRV) glycoproteins gp50,		
CC	gp63, gI and their corresponding DNA molecules. These glycoproteins are		
CC	used as vaccines for protecting animals against PRV infection.		
CC	The invention also relates to methods for protecting animals against PRV		
CC	infection. The present sequence is Pseudorabies virus (PRV) glycoprotein		
CC	animals. The present sequence is Pseudorabies virus (PRV) glycoprotein		

[illegible]

CC occurred to restore the giv-pos. phenotype. The mutant is used
CC for (multivalent) vaccine manufacture.

XX
SQ Sequence 317 AA;

Query Match 7.7%; Score 143; DB 16; Length 317;

Best Local Similarity 27.0%; Pred. No. 2.2e-05; Mismatches 123; Indels 26; Gaps 12;

Matches 68; Conservative 35; Mismatches 123; Indels 26; Gaps 12;

DB 1 MASLGLTALLATLAPFGAMGIVITGNHVSARIDDDHIVAPREPTIQL--QLFPM 58

DB 1 MRLLLMVLLAARAP--ARSLVREGAVGLADGVAFVAP--IDATLALGRLLFE 57

DB 59 GARP-HKPYSGTVAVAFRSDITNOCYOESEERFENCNHRSSVFGCKVETFFSASNR 117

DB 58 HQLPAGRRYNGTVEL--LRHYAGDCFVMLQDTAFASCPRVANDAFRCLHADTRPARSER 116

DB 118 LTGP--PHPKLTIRNRPDNGMFYIVRL---DDTKETIVFAQLSVYQFAN---- 167

DB 117 RASAAVENHVLFSIARRPRIDSLFLRVGIYGTAGSERRRVFPPLAATVSHFGEGRDP 176

DB 168 --TAATRGLYS--KACRTFGLPTVOLAVLRTEESWRNQAVYA--TEATTSAEATTP 222

DB 177 EAAAHPRGTYEAVRNCER--GLDASSASLY---DALAAFPAGAAATTPGTASSEGAAT 232

DB 223 PYTATSASELA 234

DB 233 PERVEDTEVEA 244

RESULT 13

ID AA04970 standard; Protein; 350 AA.

AC AA04970;

DT 26-SEP-2001 (first entry)

DE Pseudorabies virus glycoprotein 63, gp63.

KW Glycoprotein 63; gp63; immunogen; vaccine; PRV; Bulbar paralysis;

KW Aujeszky's disease; mad itch.

OS Pseudorabies virus.

FX Key Location/Qualifiers

FT Misc-difference 117 /note= "Encoded by GAG"

FT Misc-difference 229 /note= "Encoded by GAG"

FT Misc-difference 232 /note= "Encoded by GAG"

FT US6251634-B1.

PD 26-JUN-2001.

PE 07-JUN-1995; 950S-0485290.

PR 20-APR-1990; 900S-0513282.

PR 28-AUG-1986; 86MO-US01761.

PR 26-NOV-1985; 85US-0801799.

PR 26-MAR-1986; 86US-0844113.

PR 16-JUL-1986; 86US-0886260.

PR 29-JUN-1987; 87US-0100817.

PA (PHMA) PHARMACIA & UPJOHN CO.

PI Petrovskis EA, Post LE, Timmins JG;

DR WPI; 2001-431968/46.

DR N-PSDB; AAS08831.

PT New recombinant DNA molecules encoding a polypeptide displaying
PT pseudorabies virus (PRV) gp63 antigenicity, useful for screening
PT animals to determine whether they are infected with PRV -
XX
PS Claim 1; Column 40; 23pp; English.

CC The sequence is the pseudorabies virus (PRV) glycoprotein 63. The
CC invention relates to isolated recombinant DNA molecules, which encode a
CC polypeptide displaying pseudorabies virus (PRV) gp63 antigenicity.
CC The DNA sequences are useful for screening animals to determine
CC whether they are infected with PRV and also for expressing the
CC glycoproteins encoded. The DNA sequences are also useful in producing
CC glycoprotein gp63, which may be used as vaccines for protecting animals
CC against PRV infection, variously called Bulbar paralysis, Aujeszky's
CC disease or mad itch. PRV infects a wide range of animals and birds and
CC is invariably fatal.

SQ Sequence 350 AA;

Query Match 7.6%; Score 142.5; DB 22; Length 350;

Best Local Similarity 22.1%; Pred. No. 2.9e-05; Mismatches 149; Indels 91; Gaps 16;

Matches 80; Conservative 42; Mismatches 149; Indels 91; Gaps 16;

DB 8 LALLATLAPFGAM--GIYITGNHVSARIDDDHIVAPREPTIQLQLFPMGQRPHP 65

DB 15 LLLAALLTALTPRVGVGLFRGAGSVHAGSAVLVPGDAPNLTIGTLFLFEGSPSN 73

DB 66 YSGTVAVAFRSDITNOCYOESEERFENCNHRSSVFGCKVETFFSASNRITGP---- 121

DB 74 YSGRVEL--LRIDPKRACRYTEYAAEYDLCPRVHHEAFRGL-----RRGRLARR 122

DB 122 ----PHPKLTIRNRPDNGMFYIVRLDDTKETIVFAQLSVYQFANATATRGGL-- 174

DB 123 ASAAVEARLLFVSRPAPDAGSYLVLRVNGT---TDLEVLTAIV-----PRGRPH 172

DB 175 ----YKASCRFTGLPTVOLAVLRTEESWRNQAVYA--ATEATTTS-----AEATTP 222

DB 173 HPTPSSADECR---PVY-----GSHWDSLRYVDPEDAVFTTPPIEPPEPTTPA 219

DB 223 PYTATSAS-----ELEAEHFTFPMLENGVDHYEPTPANENSNVVRIGTMSPTLIGVT 275

DB 220 PPRGTGATPGPRSDDEEED-----EGATVTMTFVPGTLDANGM---VLNAAVSVRV 269

DB 276 VAAVVSATIG-----LVIVISIVTRNCTPHRKLDIVSODDEERSQTRRES 321

DB 270 LLAANAATAGARGPKRIAMVLGPTIVLLIFLGVCACARCARGIASGRDPGAARRST 329

DB 322 RK 323

DB 330 RR 331

RESULT 14

ID AAB82502 standard; Protein; 350 AA.

AC AAB82502;

DT 05-SEP-2001 (first entry)

DE Pseudorabies virus glycoprotein gp63.

KW PRV; glycoprotein; gp50; vaccine; diagnosis.

OS Pseudorabies virus.

FX Key Location/Qualifiers

FT Misc-difference 79 /note= "encoded by GAG"

FT Misc-difference 229 /note= "encoded by GAG"

FT US6255078-B1.

```

XX 03-JUL-2001.
PD
XX 07-JUN-1995; 95US-0485289.
XX
XX 20-APR-1990; 90US-0513282.
XX 21-JUN-1994; 94US-0262813.
XX 28-AUG-1986; 86US-0501761.
XX 26-MAR-1986; 86US-0844113.
XX 16-JUL-1986; 86US-0886260.
XX 29-JUN-1987; 87US-0100817.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Petrovskis EA, Post LE, Timmins JG;
XX
XX WPI: 2001-432046/46.
XX
XX N-PSDB; AAF90626.
XX
XX New recombinant DNA for screening animals actively infected with
XX pseudorabies virus (PRV), or for producing proteins useful as a vaccine
XX for protecting animals against PRV infection
XX
XX Example 3; Column 21-24; 21pp; English.
XX
XX The present sequence is that of pseudorabies virus (PRV)
XX glycoprotein gp63. The invention provides PRV gp50, gp63 and gI
XX glycoproteins (see AAB82501-03) and polynucleotides (see
XX AAF90623-27), and transformed host cells (especially CHO, yeast
XX and Escherichia coli) used to produce the polypeptides. Also
XX provided are subunit vaccines for PRV, methods for protecting
XX animals against PRV infection and methods for distinguishing
XX between infected and vaccinated animals. Commercial vaccine PRVs
XX have been found to have the gI and gp63 genes deleted. The gI and
XX gp63 polypeptides can therefore be used as diagnostic agents to
XX distinguish between animals vaccinated with these commercial
XX vaccines and those infected with the virulent virus.
XX
XX Sequence 350 AA:
XX
XX Query Match 7.6%; Score 141.5; DB 22; Length 350;
XX Best local Similarity 22.8%; Pred. No. 3.7e-05;
XX Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
XX
XX 8 LALLAATLAPPGAM--GIVITGNHVSARIDDDHIVYAPREATIOLQLEFMPGGRPKR 65
XX 15 LLLAALTLAALPRYGCIVLFRGAAYVHAGSAVLPQDANLITDGLLEGPSPSN- 73
XX 66 YSGTVAVAFRSDITNOCYOELESEERFENCTHRSSSVFGC--KYTEYTFAS-----NRL 118
XX 74 YSGRVGL-LRDPKRACTTREVAAEYDLCPRVHNAFAGCLRKREPLARRASAAVARRL 132
XX 119 TGPPEFKLITRNPRPDSGMFYIVRLDTEKEPIDVAIOLSYOFANTATRGL----- 174
XX 133 -----LEVSRAPPDAGSYLVRVNGT--TDLVLTALV-----PPGRPHHP 174
XX 175 --YSKASCTFGLPTVOLEAVLKTESMRNMOAYV--ATEATYTS-----AEATYTPPV 224
XX 175 TPSSADECK---PVY-----GSMHDSLRVVDPEADVFTPTTPEPPPTPAP 221
XX 225 TATSAS-----ELEAEHFTFMLENGVDHETTPAENSNTVRLGTSPTLIGTVA 277
XX 222 RGTGATPGPRSDDEEDE-----EGATTAATPVPGYLDANGTM--VYNASVYSRYVL 271
XX 278 AVVSATIG-----LVIVISIVFRNMCTPRARKIDVYSODEERSOTREESRK 323
XX 272 AAAMTAGARPGKIANVLGPTIVLLIFLGVCACARRCARGIASTGRDPCGAARRSTRR 331
XX
XX RESULT 15
XX AAR48063
XX ID AAR48063 standard; Protein; 380 AA.

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```

AC AAR48063:
XX 20-JUL-1994 (first entry)
XX
XX Sequence of polypeptide encoded by the first open reading frame in
XX the unique short (us) region of bovine herpes virus (BHV) genome.
XX
XX Insertion region; unique short region; US; vaccine; antigen.
XX
XX Bovine herpes virus type 1, strain ST.
XX
XX MO9400586-A.
XX
XX 06-JAN-1994.
XX
XX 25-JUN-1993; 93MO-FR00642.
XX
XX 26-JUN-1992; 92FR-0007930.
XX
XX (INMR ) RHONE MERIEUX SA.
XX
XX Audonnet JF, Legasteleis ICMA, Leung-tack P, Riviere MEA;
XX
XX WPI: 1994-02622/03.
XX
XX N-PSDB; AA033350.
XX
XX New insertion region sequence of bovine herpes virus genomic DNA
XX used for recombinant virus with this region deleted or
XX inactivated; useful in vaccines allowing differentiation between
XX vaccinated and infected cattle
XX
XX Claim 9; Fig 2; 47pp; French.
XX
XX The 4190 bp sequence in AA055350 encodes polypeptides homologous to
XX HSV-1 gI, gE and US9; these are neither essential for in vitro
XX replication nor important in inducing a protective immune response.
XX It is genomic DNA purified from the ST strain of BHV-1. (BHV is also
XX known as infectious bovine rhinotracheitis virus.) The sequence
XX forms the insertion region in genomic DNA. rBHV in which the
XX specific insertion region, esp. nucleotides 172-1311, has been
XX deleted or inactivated by insertion are claimed.
XX
XX Sequence 380 AA:
XX
XX Query Match 7.5%; Score 140.5; DB 15; Length 380;
XX Best local Similarity 25.3%; Pred. No. 5.2e-05;
XX Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;
XX
XX 1 MASLIGTLLAATLAPPGAMGIVITGNHVSARIDDDHIVYAPREATIOLQLEFMP 58
XX 1 MRCLLMAYVLAARAP--ARSIVRGEAVGLADPVAFAVHP--TDATILAKRLIFLE 57
XX 59 GQRP-HKPTSGIVRAFRSDITNOCYOELESEERFENCTHRSSSVFGCKYETFFSARN 117
XX 58 HOLPAGRRINGVEL-LRIHAAGDCEYMLDTTAFASCPRVANNARSCLAADTRPARSER 116
XX 118 LTGP--PHPEFKLITRNPRPDSGMFYIVRL---DTEKEPIDVAIOLSYOFA----- 166
XX 117 RASAAVENHVLFSIARPPRIDSGLYELRVAYIGTAGSERRRDVPPLAAFHSGEGDDP 176
XX 167 -----NTAATRGLYSKASCTFGL-----PTVOLEAVLKTESMR 201
XX 177 EAARTPPARSRASGLTSSASLYDRALARSPOAPPAPPARAARAPRPERVDE 236
XX 202 NMQAYVATEATTTSAEATTPTPTVATAS 230
XX 237 TTEVEAATRAGSALFTTPPAGPTASPA 265
XX
XX Search completed: May 5, 2003, 16:12:58
XX Job time : 56.5 secs

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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:11:13 ; Search time 19.5 Seconds

(Without alignments)
546,210 Million cell updates/sec

Title: US-09-993-777-68

Sequence: 1 MASLGLTALLAATLAPGANGI...VELVAIVNSALSSPSIKW 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

Issued Patents:AA:*
1: /cgn2_6/prodata/1/aaa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/aaa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/aaa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/aaa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/aaa/PCrus.COMB.pep:*
6: /cgn2_6/prodata/1/aaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	5	PCT-US96-03916-7
2	1863	100.0	362	5	Sequence 7, Appl
3	152	8.2	355	4	PCT-US96-03916-68
4	148	7.9	317	2	Sequence 28, Appl
5	148	7.9	364	1	Sequence 56, Appl
6	148	7.9	364	4	Sequence 10, Appl
7	145	7.8	370	3	Sequence 10, Appl
8	143.5	7.7	350	6	Sequence 10, Appl
9	140.5	7.5	380	4	Sequence 2, Appl
10	112	6.0	387	4	Sequence 2, Appl
11	108	5.8	713	1	Sequence 63, Appl
12	108	5.8	713	4	Sequence 63, Appl
13	108	5.8	713	4	Sequence 63, Appl
14	108	5.8	713	4	Sequence 63, Appl
15	108	5.8	713	4	Sequence 63, Appl
16	107.5	5.8	100	3	Sequence 27, Appl
17	107.5	5.8	100	3	Sequence 27, Appl
18	103.5	5.6	94	1	Sequence 6, Appl
19	103.5	5.6	94	1	Sequence 6, Appl
20	103.5	5.6	94	1	Sequence 6, Appl
21	99	5.3	97	2	Sequence 25, Appl
22	99	5.3	97	3	Sequence 25, Appl
23	98	5.3	503	1	Sequence 2, Appl
24	98	5.3	503	2	Sequence 2, Appl
25	98	5.3	503	2	Sequence 2, Appl
26	97	5.2	1220	2	Sequence 36, Appl
27	93.5	5.0	878	4	Sequence 2, Appl

28	93.5	5.0	907	3	US-08-783-774-2	Sequence 2, Appl
29	93.5	5.0	907	4	US-09-328-599A-1	Sequence 1, Appl
30	93.5	5.0	907	5	PCT-US95-04611A-19	Sequence 19, Appl
31	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl
32	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl
33	92.5	5.0	547	1	US-08-433-010-1	Sequence 1, Appl
34	92.5	5.0	547	1	US-08-482-882-1	Sequence 1, Appl
35	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
36	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
37	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
38	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
39	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
40	92.5	5.0	547	2	US-08-483-589-1	Sequence 1, Appl
41	92.5	5.0	547	3	US-08-863-790-1	Sequence 1, Appl
42	92.5	5.0	547	3	US-08-863-790-1	Sequence 1, Appl
43	92.5	5.0	547	4	US-08-475-680-1	Sequence 1, Appl
44	92.5	5.0	547	4	US-08-296-749-1	Sequence 1, Appl
45	90.5	4.9	518	4	US-09-591-435-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
PCT-US96-03916-7
Sequence 7, Application PC/TUS9603916
GENERAL INFORMATION:
APPLICANT: Wild, Martha A.
TITLE OF INVENTION: RECOMBINANT INFECTIONS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-03916-7
Query Match 100.0%; Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2; Se-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MASLGLTALLAATLAPGANGIIVTNSARIDDDHIVAPRPATIDLOLFFMPQ 60
DB 1 MASLGLTALLAATLAPGANGIIVTNSARIDDDHIVAPRPATIDLOLFFMPQ 60

QY 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFSSASNLTG 120
Db 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFSSASNLTG 120
QY 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
Db 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
QY 181 RTFGLPTVOLEAYLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
Db 181 RTFGLPTVOLEAYLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
QY 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGTVAAVVSATIGLVIYISITRNMCTP 300
Db 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGTVAAVVSATIGLVIYISITRNMCTP 300
QY 301 HRKLDIVSODDEERSQTRRESRKFGPMVACEINKGADQSELVELVAIVNPSALSSPDS1 360
Db 301 HRKLDIVSODDEERSQTRRESRKFGPMVACEINKGADQSELVELVAIVNPSALSSPDS1 360
QY 361 KM 362
Db 361 KM 362

RESULT 2

PCT-US96-03916-68
Sequence 68, Application PC/TUS9603916

GENERAL INFORMATION:

APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-03916-68

Query Match 100.0%; Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2,5e-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLTALLAATLAPFGAMGIVITGNHVSARIIDDHIVAPRREATIQLQLFPMQ 60
Db 1 MASLGLTALLAATLAPFGAMGIVITGNHVSARIIDDHIVAPRREATIQLQLFPMQ 60
QY 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFSSASNLTG 120
Db 61 RPHKPYSGTVRAVAFRSDITNOCYQELSEERFENCOTHRSSSVFGCKVTEYTFSSASNLTG 120
QY 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
Db 121 PPHPKFTITNPRPNDSGMVYIVRLDDTKEPIDVFAIOLSVQFANTATRLYSKASC 180
QY 181 RTFGLPTVOLEAYLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
Db 181 RTFGLPTVOLEAYLRTESRNNOAVYATATTSATPTPTATTSASELEAEHFTFP 240
QY 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGTVAAVVSATIGLVIYISITRNMCTP 300
Db 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGTVAAVVSATIGLVIYISITRNMCTP 300
QY 301 HRKLDIVSODDEERSQTRRESRKFGPMVACEINKGADQSELVELVAIVNPSALSSPDS1 360
Db 301 HRKLDIVSODDEERSQTRRESRKFGPMVACEINKGADQSELVELVAIVNPSALSSPDS1 360
QY 361 KM 362
Db 361 KM 362

RESULT 3

US-08-709-731A-28

Sequence 28, Application US/08709731A

Patent No. 6322780

GENERAL INFORMATION:

APPLICANT: Lee, Lucy F.
APPLICANT: Mazerian, Keyvan
APPLICANT: Wilter, Richard L.
APPLICANT: Wu, Ping
APPLICANT: Yanagida, No. 63227800ru
TITLE OF INVENTION: Marek's disease Virus Genes and Their
TITLE OF INVENTION: Use in Vaccines for Protection Against Marek's Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: VA
COUNTRY: US
ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,731A
FILING DATE: 05-JUL-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/499,474
FILING DATE: 07-JULY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1644-110FPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant


```

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Marek's disease virus type I
STRAIN: GA
FEATURE:
NAME/KEY: Protein
LOCATION: 1..355
OTHER INFORMATION: /label=protein
OTHER INFORMATION: /note="g1 protein"
US-08-709-731A-28

Query Match      8.2% Score 152; DB 4; Length 355;
Best Local Similarity 22.9%; Pred. No. 1.2e-07;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;

19 GAMGIYTGNNHSARIDDDHIYVAPRPE-ATIQLOLEFMPGQRPKPYSGTVRVAFRSD 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
15 GIMSIYTGIVTLSTDOSALVAFGCLDKAVNRQQLFLDQTRTSYTGTEI-LKMD 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 78 ITNCCYOELSEERFENCNTHSSVFVGCCKVTEYTSASRLTGPPHFK---LTINRPP 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 EBYKCSVLAHATSYMCDPAIDATVRCGRDAVVYAOPHDKV--QPPKGTLLRIYEPV 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 NDSGMFYVIRLDTRKEPIDVFAIOLSYQFANTAFRLGYSKASCTFGLPTVQLEAVL 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 SDTGSYIRVVALAG--RNMSDIFRMAVIRIS-----SKSWACHSASSFOAHKCI 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 195 RTEE--SMRMQAVYATVTEATVTSAEATTPPVATTSASELEAHEFTPEWLENGVDHYEPT 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 180 RYVDRMAFENYTLIGHGNLSDSELAHYNITPOSIS--TDINITTPPEYDNGSTIYSP 238
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 253 P---ANENSNTVRLGT-MSPLIGVVAHV--SATIGLVV--ISIVTRNCKTPHKK 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 239 VENLFNNNSHVADAMSTGMMNVLKYLPLRIYFSMIYLCIALAIYVCEKRCRSPHR 298
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 LDTYSODEERQTRRESKRFQPMVACINFGADQDSELYE 344
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 299 I----YIGPRPDE-----APLITSAVNESFQYDYNVE 328
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
US-08-344-833-2
; Sequence 2, 5874280
; Patent No. 5874280
GENERAL INFORMATION:
APPLICANT: Kell, G nther
TITLE OF INVENTION: Recombinant Bovine Herpesvirus
TITLE OF INVENTION: Vaccine
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Organon Teknika Corporation
STREET: 1330-A Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,833
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Blackstone, William B.
REGISTRATION NUMBER: 29 772
TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-344-833-2

Query Match      7.9% Score 148; DB 2; Length 317;
Best Local Similarity 27.1%; Pred. No. 2.7e-07;
Matches 68; Conservative 34; Mismatches 125; Indels 24; Gaps 11;

QY 1 MASLIGTLALATLAPFGAMGIYTGNNHSARIDDDHIYVAPRPEATIQ--OLEFMP 58
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MRLLIMVVAIAAAP--ARSLVGEAVGLRADGVAFVAPR-ITDAILARGLIFLE 57
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 59 GQRP-HKPYSGTVVAFRSDITNCCYOELSEERFENCNTHSSVFVGCCKVTEYTSASNR 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 58 HOLPAGRRYNGTVEL-LRYHAAGDCEVMLQTTAFASCPRVANDAFRSCLAADTRABER 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 118 LTGP--PHPEKLTIRNRPNDGMEYIVRL---DTKEPIDVFAIOLSYQFAN---- 167
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 117 RASAVERNVLFSIARPPIDSGLYFLRGITGTAISERRRDVFLAFAVHSFGEPDP 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 168 --TAATRGLYS--KASCTFGLPTVQLEAVLFTESWMNQAVYATBATTTSAEATTP 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 177 EAAAHPTGVEAVEARCR-GLDASSASLYDRALAFAGAA--TTPGPASSSEGAATP 233
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 224 VTATSAELEA 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 234 ERVDETTEVA 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-08-680-726A-56
; Sequence 56, Application US/08680726A
; Patent No 580167
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESS: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coonell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-680-726A-56

```

Query Match 7.98; Score 148; DB 1; Length 364;
Best Local Similarity 27.38; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

QY 4 LIGTLALLAATLAFGAMGIYITGNHVSARIDDDHIYVAPREATTQLOLFMPGQR-P 62
DB 16 LITMPLPILFLYGVNGFYKGTYSIMPLNTSSGFSIFPDDKFTYSGRLFLDDOHL 75
QY 63 HKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSVEFGC--KYTEYFASNRLTG 120
DB 76 VNNVSGTIEFT--HFNNSCYTVOTIEYFSCPRIFNNAFSCIAKYSKHHSOLRINSS 132
QY 121 PPHPEKLTIRNPNRNSGMFYIVRLDDTKEPIDVFAIQLSVYOF 165
DB 133 IENGVLLEITNPKPNDSGVYFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 6
US-09-092-409-56
Sequence 56, Application US/09092409
Patent No. 6159478

GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-092-409-56

Query Match 7.98; Score 148; DB 4; Length 364;
Best Local Similarity 27.38; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

QY 4 LIGTLALLAATLAFGAMGIYITGNHVSARIDDDHIYVAPREATTQLOLFMPGQR-P 62
DB 16 LITMPLPILFLYGVNGFYKGTYSIMPLNTSSGFSIFPDDKFTYSGRLFLDDOHL 75
QY 63 HKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSVEFGC--KYTEYFASNRLTG 120
DB 76 VNNVSGTIEFT--HFNNSCYTVOTIEYFSCPRIFNNAFSCIAKYSKHHSOLRINSS 132

QY 121 PPHPEKLTIRNPNRNSGMFYIVRLDDTKEPIDVFAIQLSVYOF 165
DB 133 IENGVLLEITNPKPNDSGVYFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 7
US-08-911-321-10
Sequence 10, Application US/08911321
Patent No. 6010703

GENERAL INFORMATION:

APPLICANT: Roger K. Maes and Stephen J. Spatz
TITLE OF INVENTION: Recombinant Foxvirus
TITLE OF INVENTION: Vaccine Against
TITLE OF INVENTION: Feline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096,183
FILING DATE: July 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: NO. 6010703e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 370
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Polypeptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Feline herpesvirus-1
STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: Deduced Sequence
OTHER INFORMATION: 91
US-08-911-321-10

Query Match 7.88; Score 145; DB 3; Length 370;
Best Local Similarity 22.08; Pred. No. 7.1e-07;
Matches 72; Conservative 52; Mismatches 136; Indels 68; Gaps 14;

QY 5 LIGTLALLAATLAFGAMGIYITGNHVSARIDDDHIYVAPRE-ATTQLOLFMPGQR-RP 62
DB 1 MSSIAFIYILMAIGTYGVIYRQDHWLSHVDTSGFVIYPTLENFTLYGHLIFLDDQRLP 60

QY 63 HKYSGTVAVAFRSDITNOCYDELSEERENCITHRSSVFGC--KYTEYTSASNRLTG 120
 DB 61 VNNYNGTLEI- IHNHSSCYKIVQIEYSSCPRRNNARSCILHTSHQDOLSTITS 119
 QY 121 PPHPEFLTIIRNRPNDGMPYIVRLDITKEPIDVFAIOLSVYOFANTAAGLYSKASC 180
 DB 120 VETGMILFTTSPKMGDGIYALVRFNHNK-ADVFGLSVFVSF-----DTGGRHHADE 174
 QY 181 RTFGA--LPTVO-LEAVLRTEESWRNMQAY--VATEATTSAEATPTPVATASAELEA 234
 DB 175 NUNGELITTPSPMETYKV-----NTPYDHVVTTOFTSNKSMESSEPSNTSISC----- 223
 QY 235 EHTEFPMLENGVDHYEPTPANENSNTVRL-----GIMSPTLIGVTAA 278
 DB 224 -----HTFQNDNBESETLYTHLNIAGNITYDDMVMDGTTLKPRLL----- 264
 QY 279 VVSATIGLVIYISIVTRMCPHRRKIDT 306
 DB 265 ----DMGLMLSTVSSFKN--GNNAKMDT 286

RESULT 8
 5352575-7
 Patent No. 5352575
 TITLE OF INVENTION: PETROVSKIS, ERIK A.; POST, LEONARD E.; TIMMINS, JAMES G.
 NUMBER OF SEQUENCES: 12
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/513,282
 FILING DATE: 20-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 100,817
 FILING DATE: 29-JUN-1987
 APPLICATION NUMBER: 886,260
 FILING DATE: 16-JUL-1986
 APPLICATION NUMBER: 784,787
 FILING DATE: 04-OCT-1985
 APPLICATION NUMBER: 801,799
 FILING DATE: 26-NOV-1985
 APPLICATION NUMBER: 844,113
 FILING DATE: 26-MAR-1986
 SEQ ID NO: 7:
 LENGTH: 350
 5352575-7

Query Match 7.7%; Score 143.5; DB 6; Length 350;
 Best Local Similarity 22.8%; Pred. No. 9.3e-07;
 Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

QY 8 LALAATLAPFGAM--GIYITGNHVSARIDDDHIVARPREATIQLOLFMPGGRPHK 65
 DB 15 LLAALTLAALPRVGVVLFRCAAVSVVAGSAVLPGDAPMLTIDGILLLEBSPSN- 73
 QY 66 YSGTVAVAFRSDITNOCYDELSEERENCITHRSSVFGC--KYTEYTSASNRL 118
 DB 74 YSGRVEL-LRLDPRACRYREYAARYDCLPRVHHAERGLRREPLARSAVAEARL 132
 QY 119 TGPHPFKLTIIRNRPNDGMPYIVRLDITKEPIDVFAIOLSVYOFANTAATG- 174
 DB 133 -----LFTVSRPAPPDAGSYVLRVNGT--TDLFVLTALV-----PPGRGRHP 174
 QY 175 --YSKASGRTFGLPVQLBAVYLRTESWRNMQAYV--ATEATTS-----AEATPTPV 224
 DB 175 PPSADECR-----PVV-----GSHWDSLRAVVDPAEDAVFTPPPIEPEPTTAP 221
 QY 225 TATSS-----ELEAEHTFPMLENGVDHYEPTPANENSNTVVALGIMSPTLIGVTA 277
 DB 222 RGTGATPEPRSDDEEDE-----EGATITAMTPVPOTILDANGTM--VLNASSVSRLL 271
 QY 278 AVVSATIG-----LVTVISIVTRMCPHRRKIDTIVSDODDEERQTRRESK 323
 DB 272 AAANATAGARGPKIAVAVLGPITVILLIFLGVAACARCARCIASGTGDCAPARRSTR 331

RESULT 9
 US-08-924-345-2
 Sequence No. 6224878
 Patent No. 6224878
 GENERAL INFORMATION:
 APPLICANT: LEONG-TACK Patricia
 APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree
 APPLICANT: AUDONNET Jean-Christophe, Francis
 APPLICANT: RIVIERE Michel, Emile, Albert
 TITLE OF INVENTION: Mutants and vaccines of the Infectious
 NUMBER OF INVENTION: Bovine Rhinotracheitis virus
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LARSON AND TAYLOR
 STREET: 727 SOUTH TWENTY-THIRD STREET
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/924,345
 FILING DATE: 04-SEP-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/199,172
 FILING DATE: 09-AUG-1994
 APPLICATION NUMBER: FR 92 07930
 FILING DATE: 26-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: SARO, THOMAS P. 10396
 REGISTRATION NUMBER: XI
 REFERENCE/DOCKET NUMBER: XI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 520-7200
 TELEFAX: (703) 892-8428
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 380 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-924-345-2

Query Match 7.5%; Score 140.5; DB 4; Length 380;
 Best Local Similarity 25.3%; Pred. No. 2.2e-06;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;

QY 1 MASLIGTLAATLAPFGAMGIYITGNHVSARIDDDHIVARPREATIQLOLFMP 58
 DB 1 MRCELLMNVVLAARAP--ARSLVRCGAVGLRADCPVAFVHP--TDATTLALRKLIFLE 57
 QY 59 GORP-HKPYSGTVAVAFRSDITNOCYDELSEERENCITHRSSVFGCKYTEYTSASN 117
 DB 58 HOLRAGRKYGYIEL-LRYHAAGDEFVLLQTVAFASCPRVANNARFSCILHDTPARSER 116
 QY 118 LTGP--TTPPKLTIIRNRPNDGMPYIVRL-----DITKEPIDVFAIOLSVYCPA----- 166
 DB 117 RASAAVENHVLFSILARPIDSGILFELVGIYGTGASGERRDVPLAFAHSVGEGRDE 176
 QY 167 -----NTAATRLGYSKASCTFG-PTVQLELYLRTESWR 201
 DB 177 EAAATPAPRSRPAASGLTSSASLYDRALARSPOAPPPRPARARAPRRPRRVE 236
 QY 202 NMQAVVATEATTSAEATPTPVATASAS 230
 DB 237 TTEVEAATRAGSAFALTTPPACPTASPA 265

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUP1, FIG. 46
US-08-477-346-63

Query Match 5.8%; Score 108; DB 4; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

DB 60 ORPHKPGYGVRAVAFSDITNOCYELSEPFENCTHRSSSVFVGCKVETFFS---AS 115
116 NRITGPPHFKITIRNPRDGMFYVIRLDITKEPI-----D 154
DB 86 QRDHQIASLTYQQQQQQQQQQQQVQOHLQQQ-QQLAASASVPAQOPATTSATATPAA 144
OY 116 NRITGPPHFKITIRNPRDGMFYVIRLDITKEPI-----D 154
DB 145 NRTTSSPAA--PVQASRNPLVGS-----QLPTTLTPVSSNAQQQLPQQQLQQQQLQQQ 197
OY 155 VFAIQLSYQANTATATGLYASACRTGRLPTVOL-EAYLFTESRMWQAVY-----A 208
DB 198 OPPQVSVAPLSNTAING--SPTSKETITLPSVKAPESTIKETEPENNNTSKINDTGA 254
OY 209 TEATTSAAET--TPPVATASASELAHFTFPMLENGVDHYEPT 253
255 TTAATTTATETEIRKREDATPAS-LHQDHYLVPINR-AHNSKPIP 299

RESULT 13
US-08-473-089-63
Sequence 63, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUP1, FIG. 46
US-08-473-089-63

Query Match 5.8%; Score 108; DB 4; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

DB 60 ORPHKPGYGVRAVAFSDITNOCYELSEPFENCTHRSSSVFVGCKVETFFS---AS 115
116 NRITGPPHFKITIRNPRDGMFYVIRLDITKEPI-----D 154
DB 86 QRDHQIASLTYQQQQQQQQQQQQVQOHLQQQ-QQLAASASVPAQOPATTSATATPAA 144
OY 116 NRITGPPHFKITIRNPRDGMFYVIRLDITKEPI-----D 154
DB 145 NRTTSSPAA--PVQASRNPLVGS-----QLPTTLTPVSSNAQQQLPQQQLQQQQLQQQ 197
OY 155 VFAIQLSYQANTATATGLYASACRTGRLPTVOL-EAYLFTESRMWQAVY-----A 208
DB 198 OPPQVSVAPLSNTAING--SPTSKETITLPSVKAPESTIKETEPENNNTSKINDTGA 254
OY 209 TEATTSAAET--TPPVATASASELAHFTFPMLENGVDHYEPT 253
255 TTAATTTATETEIRKREDATPAS-LHQDHYLVPINR-AHNSKPIP 299

RESULT 14
US-08-487-072A-63
Sequence 63, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:09:18 ; Search time 15.5 Seconds
(without alignments)
2245.204 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1863

Sequence: 1 MASULGTLALLATLAPGCA.....VELVAIVNPSALSPDSIKM 362

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	164	8.8	420	2	T42616	envelope protein -
2	162.5	8.7	334	1	VG8B67	glycoprotein D pre
3	155	8.3	353	1	C46113	glycoprotein D pre
4	153.5	8.2	424	1	VG8B69	glycoprotein gp63
5	143.5	7.7	350	2	VG8B63	glycoprotein I - b
6	140.5	7.5	380	2	S53785	glycoprotein I - b
7	125	6.7	356	2	U02352	probable glycoprot
8	124.5	6.7	683	2	T03146	probable glycoprot
9	115	6.2	457	1	RW8574	glycoprotein I pre
10	113.5	6.1	390	1	Q08E77	glycoprotein I pre
11	111.5	6.0	149	2	A61162	hypothetical prote
12	108.5	5.8	355	2	CJ9725	WD-40 repeat I pre
13	108	5.8	713	2	JN0133	glycoprotein I pre
14	107	5.7	372	2	Q08E88	glycoprotein I pre
15	99	5.3	372	2	F43674	US7 protein - hma
16	99	5.3	1036	2	S73601	protein P200 - Myc
17	98.5	5.3	1140	2	S73786	hypothetical prote
18	98	5.3	503	2	B38745	cell adhesion mole
19	98	5.3	507	2	S64507	probable membrane
20	97	5.2	1220	2	S48387	SLM1 protein - yea
21	96.5	5.2	814	1	A39752	fibroblast growth
22	95.5	5.1	797	1	VG8E61	glycoprotein X pre
23	95.5	5.1	867	2	T45463	membrane glycoprot
24	95	5.1	1777	2	T34369	hypothetical prote
25	94	5.0	796	2	T21460	hypothetical prote
26	93.5	5.0	645	2	T29818	hypothetical prote
27	93.5	5.0	907	1	Q08E21	membrane antigen g
28	93.5	5.0	3020	2	A43932	mucin 2 precursor,
29	93	5.0	1051	2	S55259	TfPI1 protein - mou

30	92.5	5.0	1778	2	AF1116	interallin protein
31	92	4.9	1044	2	E95375	probable drug resi
32	91.5	4.9	510	2	T47374	hypothetical prote
33	91	4.9	365	2	A34424	CD44 membrane gly
34	91	4.9	836	2	S49940	cell division cont
35	90.5	4.9	547	1	S28904	intercellular adhe
36	90.5	4.9	785	2	T37329	probable oligopept
37	90.5	4.9	786	2	T19017	hypothetical prote
38	90.5	4.9	1429	2	T41699	hypothetical prote
39	90	4.8	233	2	C84193	hypothetical prote
40	90	4.8	788	2	T34248	hypothetical prote
41	89.5	4.8	826	2	G90283	hypothetical prote
42	89.5	4.8	866	2	T45462	membrane glycoprot
43	89.5	4.8	992	2	T38817	hypothetical prote
44	89	4.8	629	2	A15155	probable peptidogl
45	89	4.8	678	2	S54308	DNA binding protei

ALIGNMENTS

RESULT 1	T42616	envelope protein - equine herpesvirus 4 (strain NS80567)
C:Species:	equine herpesvirus 4	
A:Variety:	strain NS80567	
C:Date:	11-Jan-2000	#sequence_Revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession:	T42616	
R:RefSeq:	E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.	
J:Gen. Virol.	79, 1197-1203, 1998	
A:Title:	The DNA sequence of equine herpesvirus-4.	
A:Reference number:	222173; PMID:98264497; PMID:9603335	
A:Accession:	T42616	
A:Stratus:	preliminary; translated from GB/EMBL/DDB3	
A:Molecule type:	DNA	
A:Residues:	1-420 <TRL>	
A:Cross-references:	EMBL:AF030027; NID:92605950; PIDN:AAC59593.1; PID:92606021	
A:Experimental source:	strain NS80567	
C:Genetics:		
A:Note:	73	
C:Superfamily:	pseudotables virus glycoprotein gp63	
Query Match	8.8%; Score 164; DB 2; Length 420;	
Best Local Similarity	25.5%; Pred No. 9.6e-06;	
Matches	96; Conservative 50; Mismatches 143; Indels 88; Gaps 21;	
OY	10 LLAATLAPGAMGIVITGNNHVSANIDDDHIVAVAPPATIOL-QLPFMRQR-PKRPYS 67	
DB	13 LLAISMCM--ATAIIVKGEHMSMTLANSSEFAVYRKOKSLVVGHMLFLDGLPLPTNYS 69	
OY	68 GTVAFAFRSDITNOCYOELESEEPENCTHRSSEVYGC--KVTETFSASNRLTGPHPF 125	
DB	70 GLIEL-IHHYNSKGCYVIGTISTESCPRVANNAFNSCLAKTSNHNDDYHNTSVETNV 128	
OY	126 KLTIRNPNDSCGMEYIVIRLDDTKRPIIDVFAIQLSVYOF-ANRAIRGLXKASGRTFG 184	
DB	129 LLNITRPOPDSGAYILRYKLNHA-PTADVGSAFVVDLOSNTVPEPVPAEPENVFT 187	
OY	185 LPTVOLAVYIRTEESWRNQAIVATEATTSAEAT--TPPTVATASSELAEHETFPW 241	
DB	188 RTPAPAPANSTK-----TGSNTWSQSSTWLYPTP-----RRA 221	
OY	242 LKNGVDHEPTPANEN--SNVTVRL-----GTMSPF-----LIGVVAVVSATIG----- 285	
DB	222 LET---HLTTAPANETVSGDTAMCHGFRPSAVPTIIMLLGLT-----GALPE 269	
OY	286 --IVIVSIYTRNMCTPHKRLDTVS-----ODDEERSQTRRSR-KFQPNV-----ACEIN 333	
DB	270 DVLLEDESELK--TPPKPQTSSRTGDEDFQKNTSTSPKSRKKIVAAVVIPTACVLM 326	
OY	334 KGADDSTVETVAIVN 350	
DB	327 -----LLIVVGAIIIN 337	

RESULT 2 VGBE67 glycoprotein D precursor - human herpesvirus 3

N:Alternate names: glycoprotein IV
C:Species: human herpesvirus 3, varicella-zoster virus
C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: F27345
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A>Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657; PMID:3018124
A:Accession: F27345
A:Molecule type: DNA
A:Residues: 1-354 <DAV>
A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27950.1; PID:g60056
C:Genetics:
A:Gene: 67
C:Superfamily: herpesvirus glycoprotein D
Keywords: glycoprotein; phosphoprotein; transmembrane protein
F:17/Domain: signal sequence #status predicted <SIG>
F:18-354/Product: glycoprotein D #status predicted <GPD>
F:279-295/Domain: transmembrane #status predicted <TMN>
F:33,47,67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted.

Query Match 8.7%; Score 162.5; DB 1; Length 354;
Best Local Similarity 22.4%; Pred. No. 1e-05;
Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

QY 23 IYTGHHVSARIDDDHIVAPPRE--ATIQQLFPMGQRP-HKPYSGTVAFRRSDI 78
DB 21 LIFGQGVSLQVNSLTSILIPQNDNYTEIKQLVFIQQLPTGTYSGTELELY-ADT 79
QY 79 TNOQYOELEERENCNHRSSVFGCKVY--EYTFSSNRLLGPHPRKLIIRNRPN 135
DB 80 VAFCEFSVOYIRIDGCPRIITSAFISCRKXKSHNIGNSDRISTEPDAGYMLITTPGIN 139
QY 136 DSGMFYVIRLDDTKEPIDVFAIQLSY-----OPANTATRGLYSKAS 179
DB 140 DAGVYVLLVLDHSRS-TDGFILGVNVYTGSHHNIHGVIYTPSLONGYSTRALFOQA- 197
QY 180 CRFGGLPT-----VLEAVLRTEES-WRNQAVYVTEATTTSAEATTPRPV 225
DB 198 -RCDLPAPRPGSGTSLFQHMIDLRAGKSLIEDNPMWLH-EDVVTETKSVKKEG----- 248
QY 226 ATSASELEAEHFTFWLENGVDHYEPTPAN-----NVTYRLGTMSPTLIGTV 276
DB 249 -----IEN---HYPTDMSTLPEKSLNDPPELLT-----IIPVA 281
DB 277 AAVVSATIGLVIVISIVTRNM 297
DB 282 SVMILTAMVIVIVISVKKRRI 302

RESULT 3
C66113
glycoprotein D precursor - cercopithecine herpesvirus 9 (strain DHV)
N:Alternate names: membrane glycoprotein 1
C:Species: cercopithecine herpesvirus 9
C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: C46113
R:Fletcher III, T.M.; Gray, W.L.
Virology 193, 762-773, 1993
A>Title: DNA sequence and genetic organization of the unique short (Us) region of the st
A:Reference number: A46113; MUID:93312509; PMID:8384754
A:Accession: C46113
A:Molecule type: DNA
A:Residues: 1-353 <FLE>
A:Cross-references: GB:I07067; NID:g310715; PIDN:AAA47888.1; PID:g310718
C:Superfamily: herpesvirus glycoprotein D
C:Keywords: glycoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-353/Product: glycoprotein D #status predicted <GPD>
F:275-293/Domain: transmembrane #status predicted <TMN>
F:40,75,84,122,138,227,252/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 8.3%; Score 155; DB 1; Length 353;
Best Local Similarity 20.2%; Pred. No. 4.2e-05;
Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11;

QY 18 FG---AMGIVITNHNVSARIDDD--HIVAPPREATIQQLFPMGQRP-HKPYSGTV 71
DB 20 FGIGCAAAIIRGNITSLVYNSATSIFLKGNNNDASIRGRFLFDGQFVTVNTVNTVE 79
QY 72 VAFRSITNOCYOELEERENCNHRSSVFGCKV-TEYTSASNRLLGPHPRKLIIR 130
DB 80 L-LHVQNTTLCLOPLRYVMGECPRIRTGAIICRYKRSWHYENATQIDRPNVEIIFKMN 138
QY 131 NRPNDSCMPYVIVRLDDTKEPIDVFAIQLSYQFANTATRLYKASCRTEGLTFYQL 190
DB 139 NIKVEDAGIYLLVVDLYT-SLFDIFVSLNVPKODTSMEDVY-----PPVYS 188
QY 191 EAV-LRTEESMRNQAVVATEATTSAEATTPRPVATSALEAEHFTFWLENGVDHY 249
DB 189 PSHILNTFKICHFPYHNGEOSILQHIY-----SDVDTEENSMQKDLGSR 238
QY 250 EPTPANENSNVTVRL-----GTMSPTLIGTVAAVVSATIGLVIVISI-VTRNMC 298
DB 239 QKPRKNFNPDKVNVNTHETKRLMESSADVEMIAVDITASLIVLIIIVVGIYRRRS 298
QY 299 TPRKIDTVSQDDEERSQTRRE 320
DB 299 SEKRKIYRPRKREQASTERE 320

RESULT 4

VGBE69
glycoprotein gp63 precursor - equine herpesvirus 1
N:Alternate names: glycoprotein I precursor; hypothetical 46k protein; ORF2 protein
C:Species: equine herpesvirus 1
A:Note: host Equus caballus (domestic horse)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: C36646; J00998; A36803
R:Audonnet, J.C.; Winslow, J.; Allen, G.; Paoletti, E.
J. Gen. Virol. 71, 2969-2978, 1990
A>Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with h
A:Reference number: A36646; MUID:91108393; PMID:2177089
A:Accession: C36646
A:Molecule type: DNA
A:Residues: 1-424 <AUD>
A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802508.1; PID:g330864
A:Experimental source: strain Kentucky D
R:Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.
Gene 101, 203-208, 1991
A>Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesvir
A:Reference number: J00998; MUID:91276272; PMID:16447559
A:Accession: J00998
A:Molecule type: DNA
A:Residues: 1-424 <ELT>
A:Cross-references: GB:M36299; NID:g330787; PIDN:AAA6547.1; PID:g330788
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.
submitted to GenBank, March 1992
A:Description: The DNA sequence of equine herpesvirus-1.
A:Reference number: A36803
A:Accession: A36803
A:Molecule type: DNA
A:Residues: 1-424 <TEL>
A:Cross-references: GB:M86664; NID:g330791; PIDN:AA802508.1; PID:g330864
A:Experimental source: strain Ab4p
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.
Virology 189, 304-316, 1992
A>Title: The DNA sequence of equine herpesvirus-1.
A:Reference number: A41831; MUID:92295566; PMID:1318606
A:Contents: annotation, possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given

C:Genetics:
 A:Gene: 73
 C:Superfamily: pseudorabies virus glycoprotein gp63
 C:Keywords: glycoprotein; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-424/Product: glycoprotein gp63 #status predicted <MNT>
 F:320-336/Domain: transmembrane #status predicted <TM1>
 F:35,67,78,121,131,236,307/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
 Best Local Similarity 23.8%; Score 153.5; DB 1; Length 424;
 Matches 70; Conservative 41; Mismatches 126; Indels 57; Gaps 12;

Db 1 MASLGLTLALATLAPFGAMGIVITGNHVSARIDDDHIVIVAPREPAITOL-QLFEPFG 59
 1 MALKTMFSAAILLSMAICSTAITYRGEHSMYLVASSEFAYFTDQSLVLGHLLEIDG 60
 60 QR-PHKYSGIVRAFRSDITNOCYOELSEERFENCTHRSSVFGC-KVTEYFSA 116
 61 QRPPTNYSGLIEI-IHYNSSVCYVLOTISTESCPRVANNARSCLEKTHHDFR 119
 117 RLTGPPHPEKLTIRNRPDSCGMFYIVRLDTPKEPIDYFAIQLSYQFANPAATRG 176
 120 VNASVETNVLNITRPPPTDSGAILLKLDNA-PRADYGVSAFYIDL- 167
 177 KASCRFFGLPTVQ---LEAVLTREESWRMOAYATATTS---AEATPPVATMSA 229
 168 KSKTVPDPMTQTQVTEPTSTVSTPYDITDVTETETESISTSQAMSTQIP-SATWG 226
 230 SELEAEHFTPEMLENGVDHYEPTPANENSNVYRIG-----TMSPTL 271
 227 TQLTTE-----LPTNE---TVISQELALCHMFQSTINPTL 260

RESULT 5
 VEBE3
 glycoprotein gp63 - suid herpesvirus 1
 C:Species: suid herpesvirus 1
 A:Note: host Sus scrofa domestica (domestic pig)
 C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999
 C:Accession: A29012
 R:Petkovskis, E.A.; Timming, J.G.; Post, L.E.
 J. Virol. 60, 185-193, 1986
 A:Title: Use of lambda phage to isolate genes for two pseudorabies virus glycoproteins w
 A:Reference number: A29012
 A:Accession: A29012
 A:Molecule type: DNA
 A:Residues: 1950 <EPT>
 A:Cross-references: GB:M14336; NID:9334055; PIDN:AAC35204.1; PID:9334056
 A:Experimental source: strain Rice
 A:Superfamily: pseudorabies virus glycoprotein gp63
 C:Keywords: glycoprotein; transmembrane protein
 F:11-72/Domain: signal sequence #status predicted <TM1>
 F:286-308/Domain: transmembrane #status predicted <TM2>
 F:56,73,153,256,262,275/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match
 Best Local Similarity 7.7%; Score 143.5; DB 1; Length 350;
 Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

Db 8 LALLATLAPFGAM-GIVITGNHVSARIDDDHIVIVAPREPAITOLQLFEPFG 65
 15 LLLALTLALTLPRVGVLEFRGAGVAVHAGAVLVGADPNLTIGTLLEFGSPSN- 73
 66 YSGIVRAFRSDITNOCYOELSEERFENCTHRSSVFGC-KVTEYFSA 118
 74 YSGRVEL-LRLDPKRCYTRVAAEYDLCPRVHNAFRGCLRRREPLARASAAVEARL 132
 119 TGPPHPEKLTIRNRPDSCGMFYIVRLDTPKEPIDYFAIQLSYQFANPAATRG 174
 133 -----LFVSRPAPDPAGSYLVLRVAVNGT---TDLEVLIALV-----PPRRP 174
 175 --YSKASCRFFGLPTVQLEAVLTREESWRMOAY--AEATPTPV 224

Db 175 TPSSADCCR-----PVV-----GSHWDLRLVDPADAEAVFTPTPEPEPTPAP 221
 225 TATSSAS-----ELAEHFTPEMLENGVDHYEPTPANENSNVYRIGTMSPTLIGVTA 277
 222 ROTGATPPRPSDEEDE-----EGATTPMTVPCTILDANGTM---VLNASVSVLL 271
 278 AVASATIG-----LVIVISIVRNKCTPRKLDVSOQDEERSQTRRSR 323
 272 AANNTANARPPCKIAMVGLPTIVLLFLGCVACARCCARGIASTGRDGAARSTR 331

RESULT 6
 S35785
 glycoprotein I - bovine herpesvirus 1
 C:Species: bovine herpesvirus 1
 C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 24-Nov-1999
 C:Accession: S35785
 R:Anderson, J.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S35782
 A:Accession: S35785
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <AND>
 A:Cross-references: EMBL:223068; NID:9312185; PIDN:CAA80605.1; PID:9312189
 C:Superfamily: pseudorabies virus glycoprotein gp63
 C:Keywords: glycoprotein

Query Match
 Best Local Similarity 7.5%; Score 140.5; DB 2; Length 380;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;

Db 1 MASLGLTLALATLAPFGAMGIVITGNHVSARIDDDHIVIVAPREPAITOL-QLFEP 58
 1 MRCLLMVAVLAAARAP--ARSLVYRGEAVGLRAGAPVAFVND-TNLTALRGRLTLE 57
 59 GQRP-HKPYSGIVRAFRSDITNOCYOELSEERFENCTHRSSVFGCCKYTEFSASNR 117
 58 HQLPACRRYNGVEL-LRYHAAGDCVMTQTAFASCPRVANNAFRCLHAQDRP 116
 118 LTGP-PHPKLTIRNRPDSCGMFYIVRLDTPKEPIDYFAIQLSYQFA----- 166
 117 RASNAVENHVLFSIRPRIDSGLYFLRVGITYGTAGSERRDVFPLAATVHSGEPDP 176
 167 -----NTAATGLYSKASCRFGL-----PYQLAVLTREESWR 201
 177 EAAARFPAPRPSRPSASLTSSASLYDRALASPPAPRPAPRAAAGPRPRPVDE 236
 202 NMOAYVTEATTTSAEATTPPTPVATMSA 230
 237 TTEVAATRAGSAFALITTPPAGPTASPA 265

RESULT 7
 J02352
 glycoprotein I - turkey herpesvirus
 N:Alternate names: ORF 7 protein
 C:Species: turkey herpesvirus
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
 C:Accession: J02352
 R:Genik, V.; Dattell, R.; Anderson, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ro
 J. Gen. Virol. 74, 2151-2162, 1993
 A:Title: The complete sequence and gene organization of the short unique region of he
 A:Reference number: J02352
 A:Accession: J02352
 A:Molecule type: DNA
 A:Residues: 1-356 <ZEL>
 C:Keywords: glycoprotein; transmembrane protein
 F:27-293/Domain: transmembrane #status predicted <TM1>
 F:154,167,230,260/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 6.7%; Score 125; DB 2; Length 356;
 Best Local Similarity 22.2%; Pred. No. 0.012;
 Matches 85; Conservative 54; Mismatches 174; Indels 70; Gaps 17;

QY 6 GTLALLATLAPF-----GAGGIYITGNHNSARIDDO-HYIVAPRPATITQLOLFEPGQ 60
 DB 5 GIACMCVTLILFCIIKTCQMYRGSLVSTYDQSAQIFEGIDIVNLYGKYLEFGDQ 64
 QY 61 RPKPYSGTVAVAFRSDITNOCYOLSEEFNCTHRSSVFCCKYTEFTFSASNLTG 120
 DB 65 YLEIYSCTMEI-LKNQANRCYSIAHATYACPIISSYFRCGRNAVYTRHSHI-- 121
 QY 121 PPHF-----FKLTIRNPDSGMEFYVRLDDTEPIDVFAIQLSYQFANTATRGLY 175
 DB 122 --HPOYNGLLITIIERPMDSGIYRTSIDGFNKS-----DYARTSIFCNG 168
 QY 176 SKASCRF-----FELPIVQ--LEAYLRTESSRMN-----QAVYATETTTSAAT 220
 DB 169 SSGSCSNPROKVSDEMCIPVNHNAIFERYLLTHVGRLPYDGLTLOQIRKMTT--APT 225
 QY 221 PTEVATASASELAEHFTFMLENGVDHYEPTPANENSNTVRLGTSPTLIGTVAAV 280
 DB 226 YRIRRTVNEGILLAKTSPDIDLNATNL-PLPI--SNT--DYMSVIMRRVALRIRY 278
 QY 281 SATIGLYIVISYTRNMCTPHRKLDTVYSDDEBSQTRRSKFG--PMVACETINKGADQ 338
 DB 279 AYLVIALIALLIVT--VCSAHKR-----GSCSRRRRIYIGNEPTLTSTINGNFQ 326
 QY 339 DSELVELVAIVNPSALSSPSIK 361
 DB 327 EKETKNV-----PSDISDAELLE 344

RESULT 8

T03146
 Probable glycoprotein A8 - alcelaphine herpesvirus 1
 C:Species: alcelaphine herpesvirus 1
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
 C:Accession: T03146
 R:Enseer, A.; Pfanz, R.; Fleckenstein, B.
 J. Virol. 71, 6517-6525, 1997
 A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
 A:Reference number: 214840; MID:97404659; PMID:9261371
 A:Accession: T03146
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-683 <ENS>
 A:Cross-references: EMBL:AF005370; NID:92337967; PIDN:AAC58098.1; PID:92338014

Query Match 6.7%; Score 124.5; DB 2; Length 683;
 Best Local Similarity 21.9%; Pred. No. 0.032;
 Matches 72; Conservative 46; Mismatches 108; Indels 103; Gaps 14;

QY 11 LAATLAPFGAMGIVITGNHNSARIDDOHYIYAPRPE-ATITQLOLFEMDGORPHRYSG 68
 DB 341 ITATTISPRGKIKAVTGNF--SRNANISLAFLSKCKEYAGVLIQA-FEESTRP--PG 394
 QY 69 TVAVAFRSDITNOCYOLSEEFNCTHRSSVFCCKYTEFTFSASNLRLGPHPEKLT 128
 DB 129 IRNPDRDSMFYIVRLDDTEPIDVFAIQLSYQFANTATRGLYSKASC----- 180
 QY 436 LITAGEHNSG-----IGSTLEPLTVSVQVLOTSPSPRDSITVYIKLTTPVODHKIV 488
 DB 181 -----RTFGLPVQLEAYLRTESSRMNQAIVYATETTTSAEANTPVPATASSEL 232
 DB 489 SPSLVTPGKRTSLPIYSMTFHSREGSSPK-----POTPAKTSSEASLPLPLTTT----- 538
 QY 233 EAEHFTFMLENGVDHYEPTPAN-----ENSNVTV-----RLGTSPTLIGV 274
 DB 539 -----PIPTNTEKSGSRFASSTVSVDTFTPGDDVNTVGTMSPS---I 577

QY 275 TVAAVSATIGLYIVISYTRNMCTPHRK 303
 DB 578 TQTLPIRTPSGROYIVY---GCCTLNR 602

RESULT 9

RMSST4
 T-cell surface glycoprotein CD4 precursor - mouse
 N:Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen T4/Len
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
 C:Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642
 R:Tourville, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R.
 Science 234, 610-614, 1986
 A:Title: Isolation and sequence of L3T4 complementary DNA clones: expression in T cell
 A:Reference number: A02110; MID:87018845; PMID:3094146
 A:Accession: A02110
 A:Molecule type: mRNA
 A:Residues: 1-457 <TOU>
 A:Cross-references: GB:M13816; NID:9192070; PIDN:AAA37267.1; PID:9309112
 R:Litman, D.R.; Gettner, S.N.
 Nature 325, 453-455, 1987
 A:Title: Unusual intron in the immunoglobulin domain of the newly isolated murine CD4
 A:Reference number: A26038; MID:87115821; PMID:3027575
 A:Accession: A26038
 A:Molecule type: mRNA
 A:Residues: 1-457 <LIT>
 A:Cross-references: GB:X04836; NID:950353; PIDN:CAA28539.1; PID:950354
 R:Gorman, S.D.; Tourville, B.; Parnes, J.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7644-7648, 1987
 A:Title: Structure of the mouse gene encoding CD4 and an unusual transcript in brain.
 A:Reference number: A39893; MID:88041159; PMID:2823269
 A:Accession: A39893
 A:Molecule type: DNA
 A:Residues: 1-25, 'E', 27-457 <GOR>
 A:Cross-references: GB:M17080; GB:J03003; NID:9192515; PIDN:AAA37402.1; PID:9387124
 R:Maddon, P.J.; Molineux, S.M.; Maddon, D.E.; Zimmerman, K.A.; Godfrey, M.; Alt, F.W.
 Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
 A:Title: Structure and expression of the human and mouse T4 genes.
 A:Reference number: A39955; MID:88097446; PMID:3501122
 A:Accession: A39955
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 25-457 <MAD>
 A:Note: the cited Genbank accession number, J03564, is not in release 101.0
 R:Parnes, J.R.; Hunkapiller, T.
 Immunol. Rev. 100, 109-127, 1987
 A:Title: L3T4 and the immunoglobulin gene superfamily: New relationships between the
 A:Reference number: I54564; MID:88152875; PMID:3326818
 A:Accession: I54564
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-457 <RES>
 A:Cross-references: GB:M36850; NID:9198670; PIDN:AAA9401.1; PID:9198671
 A:Accession: I69018
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 208-318 <RE2>
 A:Cross-references: GB:M36851; NID:9198672; PIDN:AAA9402.1; PID:9554183
 R:Classon, B.J.; Tsagaratos, J.; Kirsztbaum, L.; Maddox, J.; Mackay, C.R.; Brandon, M.
 Immunogenetics 23, 129-132, 1986
 A:Title: The L3T4 antigen in mouse and the sheep equivalent are immunoglobulin-like.
 A:Reference number: A47642; MID:86166694; PMID:3082751
 A:Accession: A47642
 A:Molecule type: protein
 A:Residues: 27-43 <CLA>
 C:Comment: This protein is expressed on most thymocytes, on a subset of mature T-cell
 C:Genetics: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2
 A:introns: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2
 C:Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
 C:Keywords: alternative initiators; duplication; immunoglobulin; T-cell; transmembrane
 F1-26; Domain: signal sequence; status predicted <SIG>
 F127-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>

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F:35-114/Domain: Immunoglobulin homology <IM>
F:139-160/Domain: Immunoglobulin homology #status atypical <IM2>
F:220-301/Domain: Immunoglobulin homology <IM3>
F:421-457/Product: CD4, Brain specific glycoprotein form #status predicted <BRA>
F:321-372/Domain: Immunoglobulin homology <IM4>
F:395-419/Domain: Transmembrane #status predicted <TM>
F:420-457/Domain: Transmembrane #status predicted <IM>
F:42-112,155-188,328-310/Duplicate bonds #status predicted
F:187,296,323,392/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 6.28; Score 115; DB 1; Length 457;
Best Local Similarity 20.68; Pred. No. 0.11;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

19 GAMGIVITGNHVSARIDDDHIVIAVPAPEPTIOLDF--PMPORPHKRYSGTVRAVR 75
Db 93 GSPLIIT-NKLKMDSOYVICELENKE-EVELWAFKTFSPGSLIDGOSLTITLDSN 149
76 SPTINOCXOEISEERENCTHSSSSVGCVEYEFSSASNLGCPHPHKKITLRNPN 135
150 SKVSN---PLTE-----CKHKKGVVSGSKV-----LSMSLRQ 181
OY 136 DSGMYIVYVRIDDTKRPIDVFIQIOLSYQVQANATRGLYSKASCRTFGPLVQLEAYLR 195
Db 182 DSDFMNCTVTITDOK--WMPFMTLSVLGQSFALR-AVKSGBSASFSPLLAFAR--- 233
OY 196 TRESRNR--MVAIVATEATTTSAAETPTPTVATSSALEAHFPEFMLENGVDHPEPT 253
234 -RNGGELIMKRA-----ENKSPFQWISFSIKNEYSV 265
OY 254 ANENSNVYVRIGTWSPLIGVVAVVASATIGLVIVISIVTNMCTPHRLKLDVSODDEE 313
Db 266 OKSTKDLKLOKLEKLPYLIKIPVSLQFAGSGN---TLTIDKTKTHQEVNLYVMKVAQ 321
OY 314 RSQTFRESRRKGFVAVCEIN-----KGADD--SELVEIYAVNPSA----- 353
Db 322 LNNIT-----LTCEWVGPTSPFKMLTLKQENQBARSEQRVQVVAPEFTGLMOQL 371
OY 354 LSSPSPIK 362
Db 372 LSGCDKVKM 380

RESULT 10
OQBET7
glycoprotein 1 precursor - human herpesvirus 1 (strain 17)
Species: human herpesvirus 1
Date: 31-Mar-1990 sequence revision 31-Mar-1990 text change 16-Jul-1999
Accession: A05243
J.McGeoch, D.J. Dolan, A. Donald, S. Rixon, F.J.
R.McGeoch, D.J. Dolan, A. Donald, S. Rixon, F.J.
F:1-390/Domain: Signal sequence #status predicted <SIG>
F:24-330/Product: glycoprotein 1 #status predicted <PI>
F:177-293/Domain: Transmembrane #status predicted <TM>
F:156,175-257/Binding site: carbohydrate (Asn) (covalent) #status predicted
A:Reference number: A00656; MOID:85160822; PMID:2984429
A:Accession: A05243
A:Molecule type: DNA
A:Residues: 1-390 <MG>
A:Cross-references: GB:L00036; NID:9291490; PIDN:AAA6661.1; PID:9291497
A:Gene: US7
C:Superfamily: herpesvirus US7 protein
C:Keywords: glycoprotein, transmembrane protein
F:1-330/Domain: Signal sequence #status predicted <SIG>
F:24-330/Product: glycoprotein 1 #status predicted <PI>
F:177-293/Domain: Transmembrane #status predicted <TM>
F:156,175-257/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 6.18; Score 113.5; DB 1; Length 390;
Best Local Similarity 20.84; Pred. No. 0.12;
Matches 72; Conservative 63; Mismatches 150; Indels 61; Gaps 15;

7 TLALATATLAPGANGIVITGNHVSARIDDDHIVIAVPAPEPTIOLDFPFGGRPHKP-65

```

27 TVSLVSNSEFDAGALG-----PDGVVEEDLLILG-----ELRFVGDDQVPHITY 69

OY 66 YGCTIVRAFAFSDITNOCCYOELSEERFENCTHRSSSVFWCKVTYEYTFASNRLTCPPHPF 125

Dh 70 YDGVVEL-WHYRPGMHCPRVVHVTATACRRPAFAAFLCADSTHS-----PAPFT 121

OY 126 -----KLTIRNRPNDSCMFYIVTLDDTKEPIDVPAIQLSYOVANPAATRGLYS 176

Dh 122 LELNIACQPLLIRQARTRDYAGYYVLFRWVGDAFN-ASLFWLAGIAABECTIAYNGSNV- 179

OY 177 KASCRTGLEDTPLYOLEVYLNTRESMRMOAAVATEATTTSABAT-PPRYTATSASELEAE 235

Dh 180 -GSCPDKLTFS--SARLAPASVYQAPANOASTPTSTSTSTTPASTTIPAD--OAS 234

OY 236 HTFFPMLE-----NGVDHEPTPANENSNTYVLGTMSPTLIQTVAAVVSATIGLYVI 290

Dh 235 TTFPTFGDPKPQPGVNHEFPs---NATRATDSRIALTVOIIQTIALTSITALIVELG 290

OY 291 STVTRNMCTPHRKLDIVSQDDERSQTRRSREKFGPMVAACEINKA 336

Dh 291 SCI-----CFIHR-----CORRYRSRRPIYSPOPTGISCAVNEMA 327

RESULT 11

A61162
glycoprotein I - equine herpesvirus 1 (strain Ab1) (fragment)
C.Species: equine herpesvirus 1
C.Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 23-Aug-1996
C.Accession: A61162
R.Elton, D.M.; Bonass, W.A.; Kilington, R.A.; Meredith, D.M.; Halliburton, I.W.
Am. J. Vet. Res. 52, 1252-1257, 1991
A>Title: Location of open reading frames coding for equine herpesvirus type-1 glycopr
A.Reference number: A61162; MUID:92027094; PMID:1656822
A.Accession: A61162
A>Status: nucleic acid sequence not shown: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-149 <ELT>
A>Note: translation of the nucleotide sequence is not complete
C:Superfamily: pseudorabies virus glycoprotein gp63
C:Keywords: glycoprotein
F:27,59,70,113,123/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.0%; Score 111.5; DB 2; Length 149;
Best Local Similarity 23.3%; Pred. NO. 0.052;
Matches 35; Conservative 33; Mismatches 69; Indels 13; Gaps 5;

OY 2 ASLGTALATLATLAFCAGCIYTGNSARIDDHIVAPREPATQL-QLFMPQG 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
2 AAILLSAIICST-----AIIYRGCHSMYLNASSEFAVYTQDSLVGLHLFFLDGG 53
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
61 R-PKRPSCGVAVAFRSDITNOCCYOELSEERFENCTHRSSSVFVC--KVETEYTFASNRL 117
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
54 RLPTTNSGIIEI-IHYNSVCTCYIQIYESCPRVANNFRSCLHTSKTHHDYFRY 112
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
118 LTGPHPFKLTIRNRPNDSCMFYIVRLD 147
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
113 NASVETNVLLINTIKPOPTSGAYTLIRKLD 142

RESULT 12
C39725
hypothetical protein (MS11 5' region) - fruit fly (*Drosophila melanogaster*)
C.Species: *Drosophila melanogaster*
C.Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Feb-1997
C.Accession: C39725
R.Samuelis, M.E.; Schedl, P.; Cline, T.W.
Mol. Cell. Biol. 11, 3584-3602, 1991
A>Title: The complex set of late transcripts from the *Drosophila* sex determination ge
A.Reference number: A39725; MUID:91260708; PMID:1710769
A.Accession: C39725
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <SAM>


```
QY 167 NTAAATRGLYSKASCRTEGLPTVQLEAYLRTESNMNQAVYATFATTSAEATPPVTA 226
      |||
Db 169 NCTFYVNGSDYSCDPAQLP-----FSAPRLGSSVYTPGASRPPT 212
      |||
QY 227 TSASELEAEHFTFPMLENGVDHYEPTPANENSNVTRLGTMSPTLIGTVAAVVSATIGL 286
      |||
Db 213 TTPSPSPRDPPTPAPG-----DTCTPAPASGERAPPNSTRSASERHRLTYAQVIOIAPA 267
      |||
QY 287 VIVISIVTRN-MCTPHRKLDTVSODDEERSQTRRESRKFGP-WVACEINKGA 336
      |||
Db 268 SIIAFVFLGSCICFIHRC-----QRRYRRPGQIYNPGVSCAVNEAA 310
      |||
```

RESULT 15

F43674
US7 protein - human herpesvirus 2 (strain HG52)

C:Species: human herpesvirus 2

Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999

Accession: F43674

MCGoch, D.J.; Moss, H.W.M.; McNab, D.; Frame, M.C.

J. Gen. Virol. 68, 19-38, 1987

A:Title: DNA sequence and genetic content of the HindIII 1 region in the short unique c
utionary comparisons.

A:Reference number: A43674; MUID:87111457; PMID:3027242

A:Accession: F43674

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <MCG>

A:Cross-references: EMBL:X04798; NID:g559900; PIDN:CAA28485.1; PID:g559906

C:Superfamily: herpesvirus US7 protein

Query Match

5.3% Score 99; DB 2; Length 372;
Best local similarity 21.0%; Pred. No. 1.8;

Matches 74; Conservative 49; Mismatches 165; Indels 64; Gaps 13;

```
QY 3 SLGTGLIATLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREAITOL-----QLEF 56
      |||
Db 5 SLGG-IATIGLWVC---ATGIIVRGPTVSL-VSDSLVAGAVGQGFVEDLAVRGELHF 59
      |||
QY 57 MGOQRHKKPYSGIVRAFRSDIINOCYQELSEERENCITHRSSSVFQGVKVTXTPSASN 116
      |||
Db 60 VCAQVPHNTYIDGIIELFHTPLGNHCPVYVHYVTLACPRPAAVATLCKSTIHANS--- 116
      |||
QY 117 RLTGPPHP-----KLTINRPNDSGMFYIVRLDP-TKEPIDVFAIOLSYQFA 166
      |||
Db 117 ----PAYFLELGLAROPLLVRATATRDYAGLYLRLVWGSATNASRFVLGVALS--A 168
      |||
QY 167 NTAAATRGLYSKASCRTEGLPTVQLEAYLRTESNMNQAVYATFATTSAEATPPVTA 226
      |||
Db 169 NCTFYVNGSDYSCDPAQLP-----FSAPRLGSSVYTPGASRPPT 212
      |||
QY 227 TSASELEAEHFTFPMLENGVDHYEPTPANENSNVTRLGTMSPTLIGTVAAVVSATIGL 286
      |||
Db 213 TTPSPSPRDPPTPAPG-----DTCTPAPASGERAPPNSTRSASERHRLTYAQVIOIAPA 267
      |||
QY 287 VIVISIVTRN-MCTPHRKLDTVSODDEERSQTRRESRKFGP-WVACEINKGA 336
      |||
Db 268 SIIAFVFLGSCICFIHRC-----QRRYRRPGQIYNPGVSCAVNEAA 310
      |||
```

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Job time : 17.5 secs

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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:06:38 ; Search time 15.5 Seconds
(Without alignments)
968.673 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1863
Sequence: 1 MASLGTALLAATAPGA.....VELVALVPSALSPPSIRKM 362

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SWISSPROT_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162.5	8.7	354	1	VGLI_VZVD
2	155	8.3	353	1	VGLI_SYVD
3	153.5	8.2	424	1	VGLI_HSEVB
4	143.5	7.7	350	1	VGLI_PSVRI
5	140.5	7.5	380	1	VGLI_HSVBS
6	115	6.2	457	1	CD4_MOUSE
7	113.5	6.1	390	1	VGLI_HSV11
8	108	5.6	713	1	TUPI_YEAST
9	107	5.7	372	1	VGLI_HSV23
10	99	5.3	1036	1	VGLI_HSV2H
11	98.5	5.3	1140	1	PD00_MYCPN
12	98	5.3	503	1	CD4_RAT
13	98	5.3	507	1	GLA4_HSEVB
14	98	5.3	1220	1	SLN1_YEAST
15	97	5.2	797	1	VGLI_HSEVB
16	95.5	5.1	907	1	VGP3_EBV
17	93.5	5.0	1051	1	TF1A_MOUSE
18	91	4.9	836	1	NOT3_YEAST
19	91	4.9	3178	1	YS89_CAEEL
20	90.5	4.9	547	1	ICAA3_HUMAN
21	90.5	4.9	785	1	CP7A_CAEEL
22	90.5	4.9	1429	1	YC31_SCHPO
23	90.5	4.9	344	1	URB6_HCMVA
24	88.5	4.8	376	1	POS_FUGRU
25	88	4.7	1037	1	VHIT_ECOLI
26	86.5	4.6	430	1	CINA_MYCTU
27	86	4.6	636	1	YNR6_YEAST
28	86	4.6	503	1	PODX_MOUSE
29	85.5	4.6	376	1	MID2_YEAST
30	85	4.6	583	1	CH12_CANAL
31	85	4.6	812	1	FGRI_XENLA
32	85	4.6	812	1	FGRI_XENLA
33	85	4.6	1718	1	RRPO_SHVX

34	84.5	4.5	440	1	T10B_HUMAN
35	84.5	4.5	678	1	VTD3_AGRHR
36	84.5	4.5	1049	1	TR45_HUMAN
37	84.5	4.5	1058	1	UR41_HUMAN
38	84.5	4.5	2738	1	PCSV_RAT
39	84.5	4.5	3376	1	ZAN_MOUSE
40	84	4.5	336	1	CM4C_RAT
41	84	4.5	1640	1	CH42_HUMAN
42	83.5	4.5	586	1	YEW4_ECOLI
43	83.5	4.5	655	1	CD44_MOUSE
44	83.5	4.5	881	1	YDH8_YEAST
45	83.5	4.5	903	1	ECIC_BOVIN

ALIGNMENTS

RESULT 1
VGLI_VZVD STANDARD; PRT; 354 AA.
ID VGLI_VZVD
AC P09258;
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glycoprotein I precursor (Glycoprotein IV) (GI) (GPV).
GN 67
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10338;
RX MEDLINE=8630657; PubMed=3018124;
RA Davidson A.O., Scott J.E.,
RT The complete DNA sequence of varicella-zoster virus.
RL J. Gen. Virol. 67:1759-1816(1986).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=84131932; PubMed=6321154;
RA MEDLINE=84131932; PubMed=6321154;
RX Davidson A.O.;
RT "DNA sequence of the US component of the varicella-zoster virus genome."
RL EMBL J. 2:2203-2209(1983).
[3]
RN MOTAGENESIS, AND PHOSPHORYLATION SITE.
RP MEDLINE=94267879; PubMed=8207795;
RA Yao Z., Grose C.;
RT "Unusual phosphorylation sequence in the gpIV (gI) component of the varicella-zoster virus gpI-gpIV glycoprotein complex (VZV gE-gI complex)."
RL J. Virol. 68:4204-4211(1994).
RN -1 SUBUNIT: HETERODIMER OF GPV AND GPI (GE).
RX -1 SUBCELLULAR LOCATION: Type I membrane protein.
RT -1 SIMILARITY: TO HERPESVIRUSES GLYCOPROTEINS I, AND TO PRV GP63.
[4]
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[5]
CC EMBL: X04370; CAA27950.1; -;
CC EMBL: X00208; CAA52032.1; -;
CC PIR: F27345; VGB67;
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01688; Herpes_gI.1.
KW Glycoprotein; Phosphorylation; Transmembrane; Signal.
FT SIGNAL 1 354
FT CHAIN 18 295 GLYCOPROTEIN I.
FT DOMAIN 18 295 POTENTIAL.
FT TRANSMEM 296 312 POTENTIAL.

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FT  DOMAIN 313 354  CYTOPLASMIC (POTENTIAL).
FT  MOD.RES 343 343  PHOSPHORYLATION.
FT  CARBOHYD 33 33  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 47 47  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 67 67  N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD 116 116  T-LINKED (GLCNAC. . .) (POTENTIAL).
FT  MUTAGEN 338 338  T->A: NO EFFECT ON PHOSPHORYLATION:
FT  MUTAGEN 341 342  EE->AA: MODERATE DECREASE IN
      PHOSPHORYLATION.
FT  MUTAGEN 343 343  S->A: MARKED DECREASE IN PHOSPHORYLATION.
FT  MUTAGEN 344 344  P->A: MARKED DECREASE IN PHOSPHORYLATION.
FT  MUTAGEN 345 345  P->A: DECREASE IN PHOSPHORYLATION.
SQ  SEQUENCE 354 AA: 39364 MW: E52B0B0B52E666 CRC64:

Query Match 8.7%; Score 162.5; DB 1; Length 354;
Best Local Similarity 22.4%; Pred. No. 2.6e-06;
Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15:

QY 23 IVTGNHVSARIDDDHIVAPRPE--ATIQQLFPMGQRP-HKPYSGTVAFRRSDI 78
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    21 LIFKGDHVSILQVNSLSLTLIPMNDNYTEIKQLVFIQDLPTGTNYSCLELLY-ADT 79
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    79 TNCYOELSEPERNCTHRSSVFGCKVT--EYTFASNRLTGPPHPEKLTIRNPRN 135
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 80 VAFCFRSVOYRIKDCGPRITSAFISCRKXKSHWHGNSIDRISTEPDAGYMLITTPGIN 139
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 136 DSGMFYVIRLDDTKEPIDVFAIQLSVY-----OPANTATRGYSKAS 179
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 140 DAGVYVLLVLDHRSR-TDGFILGVNVYTGSHHNIHGVIYTSPLQNGVSTRALRQA- 197
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 180 CRFGFLPT-----VLEAVLRTEES-WRNMQAVYVTEATTTSAAETTPPVY 225
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 198 -RUCDLPATPKSGTSLFQHMLDLRAGKSLSDNPMLH-EDVYTTETKSVYKEG----- 248
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 226 ATASELEAEHFFPMLNCGVDHYEPTPAN---ENS-----NVTYRLGMSPTLIGTV 276
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 249 -----IEN---HYPTDMSTLPEKSLNDPENLLI-----IIPVA 281
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 277 AAVVSATIGLVISIVTRNM 297
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 282 SVMILTAMVIVIVISVRRRI 302
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

RESULT 2
VGLI_SVVD STANDARD: PRT: 353 AA.
ID VGLI_SVVD 004547;
AC 004547;
DT 01-JUN-1994 (Rel. 29, Created)
RT 01-JUN-1994 (Rel. 29, Last sequence update)
RL 01-OCT-1996 (Rel. 34, Last annotation update)
OS Glycoprotein 1 precursor (Membrane glycoprotein 1).
GN GI OR US3.
OS Simlan varicella virus (strain DHV) (Cercopithecine herpesvirus 9).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_Taxid=36348;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9312509; PubMed=8384754;
RX Fletcher T.M. III, Gray W.L.;
RT "DNA sequence and genetic organization of the unique short (US)
RT region of the simlan varicella virus genome.";
RL Virology 193:762-773(1993).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS 1, TO VZV GP1V,
CC AND TO PRV GP63.
CC -----
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CC  -----
CC  EMBL: L07067; AAA47888.1; -
DR  PIR: C46113; C46113.
DR  InterPro: IPR002874; Herpes_g1.
DR  Pfam: PF01688; Herpes_g1.
KW  Glycoprotein; Transmembrane; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 353
FT  DOMAIN 21 274
FT  TRANSMEM 275 293
FT  DOMAIN 294 353
FT  CARBOHYD 40 40
FT  CARBOHYD 75 75
FT  CARBOHYD 84 84
FT  CARBOHYD 122 122
FT  CARBOHYD 138 138
FT  CARBOHYD 227 227
FT  CARBOHYD 252 252
SQ  SEQUENCE 353 AA: 40470 MW: E0314F7B5B0E4AA2 CRC64:

Query Match 8.3%; Score 155; DB 1; Length 353;
Best Local Similarity 20.2%; Pred. No. 1.1e-05;
Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11:

QY 18 FG---AMGITGNHVSARIDDD--HIVAPRPEATIQQLFPMGQRP-HKPYSGTVR 71
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 20 FGICQAAAIIRNGYISLVYNSATSIFLKGNNNDASIRGRFLFIDQFVTVYNTV 79
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 72 VAFRSITNOCYOELSEPERNCTHRSSVFGCKV-TETTFASNRLTGPPHPEKLTIR 130
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 80 L-LHVNOTLTCLQPLRYVMGECPRITGAIACRVKRSNHYNAQQLDNPVEIIFKKN 138
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 131 NRPNDGMPFYVIRLDDTKEPIDVFAIQLSVYQFANTATRGYSKASCRTPGLPTVOL 190
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 139 NTKVEDAGIILLVQDYLT-SLFDIFFVSLNVPKQDTSMDVNY-----FFPVYS 188
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 191 EAV-LRTESWRNQAVVATEATTTSAAETTPPVATSASELEAEHFFPWLNGVDHY 249
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 189 PSHILNTFKCHKFPVHNGMEOSILOHIVP-----SDVDTETENISMOKDLGSR 238
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 250 EPTPANENSVNRYRL-----GTMSPTLIGTVAAVVSATIGLVISY-VTRNNC 298
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 239 QKPRKNFNPDKVKNVTHETKTLMESSADYFMIAVPTASLVITLIIIVVGIYRRRS 298
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    QY 299 TPHRKLDIVSQDDERSQTRRE 320
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
    DB 299 SEKRKIYRPRKTRKQASTEKRE 320
    :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::

RESULT 3
VGLI_HSVB STANDARD: PRT: 424 AA.
ID VGLI_HSVB 18553;
AC 18553;
DT 01-NOV-1990 (Rel. 16, Created)
RT 01-NOV-1990 (Rel. 16, Last sequence update)
DL 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glycoprotein 1 precursor.
GN GI OR 73.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1),
OS Equine herpesvirus type 1 (strain ABI) (EHV-1), and
OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_Taxid=31520, 10328, 10330;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Ab4p;
RX MEDLINE=92295566; PubMed=1318606;
RT Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).

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RP SEQUENCE FROM N.A.
 RC STRAIN-ABI;
 RX MEDLINE-91276272; PubMed-1647359;
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
 RA Bonass W.A.;
 RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
 RT herpesvirus type-1 short unique region.";
 RL Gene 101:203-208(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Kentucky D;
 RX MEDLINE-91108393; PubMed-2177089;
 RA Audonnet J.-C., Winslow J., Allen G., Paolletti E.;
 RT "Equine herpesvirus type 1 unique short fragment encodes
 RT glycoproteins with homology to herpes simplex virus type 1 gD, gI and
 RT gE.";
 RL J. Gen. Virol. 71:2969-2978(1990).
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
 CC AND TO PRV GP63.
 CC
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 CC
 CC EMBL; M86664; AB02508.1; -;
 DR EMBL; M36299; AAA6547.1; -;
 DR PIR; C36646; VGBEE9.
 DR PIR; J00998; J00998.
 DR PIR; A36803; VGBEG4.
 DR InterPro: IPR002874; Herpes_gI.
 DR Pfam: PF01688; Herpes_gI; 1.
 KW Glycoprotein; Signal; Transmembrane.
 FT CHAIN 1 22 POTENTIAL.
 FT SIGNAL 23 424 GLYCOPROTEIN I.
 FT DOMAIN 23 319 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 320 340 POTENTIAL.
 FT DOMAIN 341 424 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 35 35 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 67 67 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 78 78 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 424 AA; 46392 MW; EE9BEFTDA895806 CRC64;
 Query Match 8.28; Score 153.5; DB 1; Length 424;
 Best Local Similarity 23.88; Pred. No. 1.9e-05;
 Matches 70; Conservative 41; Mismatches 126; Indels 57; Gaps 12;
 OY 1 MASLLGLTLLAATLAPFGAMGIVITGNVHSARIDDDIYVAPRPATLOLQLEFMNG 59
 DB 1 MAKLTGMSAAILLSMAICSTAIITIRGEHSMKLNLSSEFAYPTDQSLVGLHLFLD 60
 OY 60 QR-PHKPYSGTVAFNRSDITNOCYOLSEERENGCTHRSSVFGCC--KVTEYTESAN 116
 DB 61 ORLPPTYNSGLIEL-IHNYSSVCYVIOFTSYSCPRVANAASFCSLHKTSTYHDER 119
 OY 117 RLTPRPFRKLITRPNRPNDSGMFYVIVRLDTRKEPIDVFAIOLSVYOFANTATRGV 176
 DB 120 VNASVETNVLNITTKPOPDSCAYILRVKLDHA-PRADVFVSARVYDL----- 167
 OY 177 KASCRFGGLPTVQ---LNAVLTRESWRNQAQVATEATTS---AEATTPPVATSA 229
 DB 168 KSKIVDPMPPTIOTVETPTSYSTPTDYDODVTEESTSTOOCAMTSTQTP-SATWG 226
 OY 230 SELAEHFTFPMLENGVDHYEPTPANENSNTVRLG-----TMSPTL 271

DB 227 TQLTTE-----LPTNE-----TVVIGGALLCHWFOPSTVPTL 260
 RESULT 4
 ID VGLT_PRIVI STANDARD; PRT: 350 AA.
 AC P07646; Rel. 07, Created
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-APR-1988 (Rel. 38, Last annotation update)
 DE Glycoprotein GP63 precursor.
 OS Pseudorabies virus (Strain Rice) (PRV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 NCBI_TaxID=10350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-86308235; PubMed-3018284;
 RA Petrovskis E.A., Timmins J.G., Post L.E.;
 RT "Use of lambda gIII to isolate genes for two pseudorabies virus
 RT glycoproteins with homology to herpes simplex virus and varicella-
 RT zoster virus glycoproteins.";
 RL J. Virol. 60:185-193(1986).
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, AND TO VZV
 CC GP1V.
 CC
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 CC EMBL; M14336; AAC35204.1; -;
 DR PIR; A29012; VGBE63.
 DR InterPro: IPR002874; Herpes_gI.
 DR Pfam: PF01688; Herpes_gI; 1.
 KW Glycoprotein; Transmembrane; OR 27 (POTENTIAL).
 FT CHAIN 1 23 GLYCOPROTEIN GP63.
 FT SIGNAL 24 350 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 24 285 POTENTIAL.
 FT TRANSMEM 286 308 POTENTIAL.
 FT DOMAIN 309 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 256 256 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAc...) (POTENTIAL).
 SQ SEQUENCE 350 AA; 36773 MW; 66AE2229EC21BEDA CRC64;
 Query Match 7.77; Score 143.5; DB 1; Length 350;
 Best Local Similarity 22.88; Pred. No. 0.0001;
 Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
 OY 8 LALLAATLAPFGAM--GIVITGNVHSARIDDDIYVAPRPATLOLQLEFMNGORPHR 65
 DB 15 LLLAALLAATLAPRIVGVLPRGAGVSVHAGSALVPGDAPRLITDGLLFLBGPSPSN- 73
 OY 66 YSGIVNARAPRSDITNOCYOLSEERFENGCTHRSSVFGCC--KVTEYTESAS-----NRL 118
 DB 74 YSGNVEL-LRDPKRCACITREYAAEDLCRVNHEAFRCCLKRPRLARRASAAVBARRL 132
 OY 119 TGRPHRKLITRPNRPNDSGMFYVIVRLDTRKEPIDVFAIOLSVYOFANTATRGV----- 174
 DB 133 -----LNVSRAPRPNDSGMFYVIVRLDTRKEPIDVFAIOLSVYOFANTATRGV-----PRGRNHR 174
 OY 175 -YSKASCRFGGLPTVQ---LNAVLTRESWRNQAQVATEATTS---AEATTPPVATSA 224
 DB 175 TPSSADCR---PVV-----GSMHSLRVNVPADAVFTTPPEPEPTTPAPR 221

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OY 225 TATSAS-----ELEHEFTFWLGVNDHYEPTPANSNTVRLGTSPLIGTVTA 277
DB 222 RGATGATPEPSDEEEDDE-----EGATGATMPVPCTLDANGM---VLTASVSVRL 271
OY 278 AVVSATIG-----LVIVISIVTRNCTPHRLDLYSODDEERSQTRRSRK 323
DB 272 AAANAATGANGPGKIAMVLPCTVLLIFLVGVAAACARCARCAGIASTGRDPAARSTR 331

RESULT 5
VGLL_HSVBS
ID VGLL_HSVBS STANDARD: PRT: 380 AA.
AC 008102;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glycoprotein I.
GN GI.
OS Bovine herpesvirus type 1.2 (strain ST1).
OC Alphaherpesvirinae; Varicelloviridae;
NCBI_TaxID=45407;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94167875; PubMed=8122370;
RA Leung-Trick P., Audonnet J.F., Riviere M.;
RT "The complete DNA sequence and the genetic organization of the short
RL unique region (US) of the bovine herpesvirus type 1 (ST strain).";
RT Virology 199;409-421(1994).
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN I, TO VZV GRTV,
CC AND TO PRV GP63.
CC
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CC
CC EMBL: 223068; CA80605.1;
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01688; Herpes_gI.
KW Glycoprotein.
FT CARBOHYD 67
FT SEQUENCE 380 AA; 39910 MW; AEBE1FB9B430D2BD CRC64;
SQ
Query Match 7.5%; Score 140.5; DB 1; Length 380;
Best Local Similarity 25.3%; Pred. No. 0.0002;
Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;
OY 1 MASLLTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREATIOL--OLEFMP 58
DB 1 MRCLLLMNVYLAARAP--ARSLVYGEAVGLRADGPAFAVAHP--TDATLALGRLIFLE 57
OY 59 GQAP-HKPSGIVRAFRSITNOQOESEEPENCNTHRSSVGVCKVETTESASN 117
DB 58 HQPAGRRRYNGVEL-LRYHAAGDCFVMLQTTAFASCPRYANNAFSCILADRRPARSER 116
OY 118 LTGP--PHPEKLTIRNRPDMSGMFYIVRL---DDTKPEIVVFAIQLSVYQFA----- 166
DB 117 KASAAVENHVLSTIARPRPDSGLYFLRVGITYGTAGSEKRRRDVFFLAFAVHSFGEGDP 176
OY 167 -----NTAATRGLYSKASCRFTGL-----PTVOLEAVYRTESMR 201
DB 177 EAAARTPARSROSRPASGITSASLYDRALANSPQAPPRAPRAAARGPRRPERVDE 236
OY 202 NMOAVATEATTTSACATPTPTTATSAS 230
DB 237 TTEVAATRAGSAFALTTPAGPTASPA 265
RESULT 6

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CD4_MOUSE
ID CD4_MOUSE STANDARD: PRT: 457 AA.
AC P06332;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE T4/Leu-3) (T-cell differentiation antigen L3T4).
GN CD4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87018845; PubMed=3094146;
RA Tourville B., Gorman S.D., Field E.H., Hunkapiller T., Parnes J.R.;
RT Isolation and sequence of L3T4 complementary DNA clones: expression
RT in T cells and brain.
RL Science 234:610-614(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87115821; PubMed=3027575;
RA Littman D.R., Gettner S.N.;
RT "Unusual Intron in the Immunoglobulin domain of the newly isolated
RL murine CD4 (L3T4) gene."
RL Nature 325:453-455(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=88152875; PubMed=3326818;
RA Parnes J.R., Hunkapiller T.;
RT "L3T4 and the immunoglobulin gene superfamily: new relationships
RL between the immune system and the nervous system."
RN Immunol. Rev. 100:109-127(1987).
RN [4]
RP SEQUENCE FROM N.A. (BRAIN FORM).
RC TISSUE=Brain;
RX MEDLINE=88041159; PubMed=2823269;
RA Gorman S.D., Tourville B., Parnes J.R.;
RT "Structure of the mouse gene encoding CD4 and an unusual transcript
RL in brain."
RL Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112780; PubMed=9445485;
RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
RA Lu J., Gorrell J.H., Chinnault A.C., Belmont J.W., Miller W.,
RA Gibbs R.A.;
RT "Comparative sequence analysis of a gene-rich cluster at human
RT chromosome 12p13 and its syntenic region in mouse chromosome 6."
RL Genome Res. 8:29-40(1998).
RN [6]
RP SEQUENCE OF 27-43.
RX MEDLINE=86166694; PubMed=3082751;
RA Claesson B.J., Tsagaratos J., Kitzbaum L., Maddox J., McKay C.R.,
RA Brandon M., McKenzie I.F.C., Walker I.D.;
RT "The L3T4 antigen in mouse and the sheep equivalent are
RT immunoglobulin-like."
RL Immunogenetics 23:129-132(1986).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=86233454; PubMed=3086886;
RA Claesson B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;
RT "Partial primary structure of the T4 antigens of mouse and sheep:
RT assignment of intrachain disulfide bonds."
RL Proc. Natl. Acad. Sci. U.S.A. 83:4493-4503(1986).
RN [8]
RP FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC [9]
CC SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC [10]
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC [11]
CC SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC [12]
CC SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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DR EMBL: M36850: AAA39401.1: -
DR EMBL: M3816: AAA37267.1: -
DR EMBL: X04836: CAA28539.1: -
DR EMBL: M36851: AAA39402.1: -
DR EMBL: M17080: AAA37403.1: -
DR EMBL: M17078: AAA37403.1: JOINED.
DR EMBL: AC002397: AAC36010.1: -
DR PIR: A02110: NMST4
DR PIR: A26038: A26038.
DR HSP: P01730: IMR.
DR MDD: MGI:88335: CD4.
DR InterPro: IPR000573: CD4_TCRg.
DR InterPro: IPR003006: Ig_MHC.
DR InterPro: IPR003600: Ig_Like.
DR InterPro: IPR003596: Ig_V.
DR Pfam: PF00047: Ig_1.
DR PRINTS: PR00692: CD4TCANTIGEN.
DR SMART: SM00410: Ig_Like_2.
DR SMART: SM00406: IGV_1.
KW Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
KW Immune response; Repeat; Signal; Lipoprotein; Palmitate;
KW Alternative splicing.
FT SIGNAL 1 26
FT CHAIN 27 457 T-CELL SURFACE GLYCOPROTEIN CD4.
FT DOMAIN 27 394 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 395 417 POTENTIAL.
FT DOMAIN 418 457 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 27 128 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 129 207 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 208 317 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 318 374 IG-LIKE C2-TYPE DOMAIN 3.
FT CARBOHYD 187 187 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT DISULFID 42 112
FT DISULFID 159 158
FT DISULFID 328 370
FT LIPID 418 421 PALMITATE (BY SIMILARITY).
FT LIPID 421 421 PALMITATE (BY SIMILARITY).
FT VARSPLIC 1 240 MISSING (IN BRAIN-SPECIFIC ISOFORM).
SQ SEQUENCE 457 AA; 51296 MW; 1B1DA7527CB00F33 CRC64.

Query Match 6.2%; Score 115; DB 1; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.035; Indels 106; Gaps 16;
Matches 76; Conservative 54; Mismatches 133;

OY 19 GAMGIVITGNHVSARIDDIHIVAPREATTIOLDF--FMDGPRPKRPSGVYRVAFR 75
DB 93 GSPPLIT--NKLKMDQSQYICELNRE--EVELMVKYFSGTSLLOGOSTLITLDSN 149
OY 76 SDITNOCVOELSEERFENCSTRSSVFGCKVTEXTESASNRLTGPHPFKLTIRNPN 135
DB 150 SKYSN---PLTE---CKHKKGVSSGSKV-----LSMNLNVQ 181
OY 136 DSGMEVYVIRLDIDDKPEIDVFAIOLSVYOFANTATIRGLYSKASCRTGLPVLQEAFLR 195
DB 182 DSDFNVCYTLIDOKK---NMFGMTLSVLGFSTAIT--AYKSEGSSEFSPINFAE--- 233
OY 196 TEESAPN--WQAYVATEITTSAAETTPPVATASASLEAEHETPFLNENGVADYEPTP 253
DB 234 -ENMGELMKKA-----EKDSFPQWISFSIKKREYSV 265

OY 254 ANENSNVTVRLGTMSPTLIGYVAAVSATIGVIVISITRNKCTPRKLDIVSODDE 313
DB 266 OKSTRKDLKLTKEPLTLTKLIPVSLQFASGNL---TLTLDKGTLLHOENLVKVAQ 321
OY 314 RSQRRRSRFRFGPMVACEIN-----KGADD---SELVELVAIVNPSA----- 353
DB 322 LNNT-----LICEVAGTSPKMRITLKQENQEARVSEQVGVAVAPETGMQCL 371
OY 354 LSSPSSIKM 362
DB 372 LSEGRKVM 380

RESULT 7
ID VGLI_HSV11 STANDARD; PRT: 390 AA.
AC P06487.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Glycoprotein I.
GN GI OR US7.
OS Herpes simplex virus (type 1 / strain 17).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10299;
RN [1]
RP MEDLINE=8516822; PubMed=2984429;
RX McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
RT "Sequence determination and genetic content of the short unique
RT region in the genome of herpes simplex virus type 1."
RL J. Mol. Biol. 181:1-13(1985).
BL 1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
BL 2: GH, GB, GC, GD, GI, AND GE.
BL -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
BL AND TO PRV GP63.
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DR EMBL: L00036: AA96681.1: -
DR EMBL: X14112: CAA32284.1: -
DR EMBL: X02138: CAA26061.1: -
DR PIR: A05243: Q0BE77.
DR InterPro: IPR002874: Herpes_g1.
DR Pfam: PF01688: Herpes_g1.
KW Glycoprotein.
FT CARBOHYD 156 156 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAG. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAG. . .) (POTENTIAL).
SQ SEQUENCE 390 AA; 41369 MW; 39381B1D65F08C8 CRC64.

Query Match 6.1%; Score 113.5; DB 1; Length 390;
Best Local Similarity 20.8%; Pred. No. 0.038; Indels 61; Gaps 15;
Matches 72; Conservative 63; Mismatches 150;

OY 7 TLIALIATAPFAMQIVITGNHVSARIDDIHIVAPREATTIOLDFMPCGRPKRP 65
DB 27 TVSLVSNFVDAGALG-----PDGVVEEDLLITG-----ELRFQDGVDPRTYV 69
OY 66 YSGIYRAVFSIDITNOCVOELSEERFENCSTRSSVFGCKVTEXTESASNRLTGPHP 125
DB 70 YDGVVEL-WHYPKQHCPRVIVVVTACPRPAVALCRATDSYHS-----PAYPV 121
OY 126 -----KLTIRNPNRPNDSGMFVYVIRLDIDDKPEIDVFAIOLSVYOFANTATIRGLYS 176
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ID	Accession	Protein Name	Length	Source
Db	122	LELNIAQPLLRLVORATRDYAGVYVLRWVGDAEN-ASLFLIGMAIAEGTLANGSAV	179	NCBI
Oy	177	KASQCTPELPVQLEAVYRTESRNNQAVATATTSNAET-PPVPRATASLELAE	235	NCBI
Db	180	GSCDPKLLPS-SAPRLAPASVQIPADNOASTSTSTTPSTTIPAPSTTIPAP-QAS	234	NCBI
Oy	236	HTEPFWLE-----NGVDHEPTPANENSNVYRLGTSPPLTIGTVAAVVSATIGLYVI	290	NCBI
Db	235	TTPFTGDPKQPQPGVNHPEPS-----NATRATRDSRALVTVQIQIAIPASIALVFLG	290	NCBI
Oy	291	SIVIRNMCTPHRKLDYVSQDDEESQTRRSRKRGPMVACEINKGA	336	NCBI
Db	291	SCI-----CFIHR-----CQRRYRSRRPRTSPQMPGTSCAVNEEA	327	NCBI

ID	Accession	Protein Name	Length	Source
RESULT 8				
TUPL1_YEAST				
AC	P16649	STANDARD: PRT: 713 AA.		
DT	01-AUG-1990 (Rel. 15, Created)			
	01-NOV-1990 (Rel. 16, Last sequence update)			
	15-DEC-1998 (Rel. 37, Last annotation update)			
	Glucose repression regulatory protein Tup1 (Flocculation suppressor protein) (Repressor ABR2).			
GN	TUPL1 OR ABR2 OR SFL2 OR CTC9 OR UMK7 OR AAR1 OR AMM1 OR FLK1 OR YCR084C OR YCR84C.			
OC	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91061758; Pubmed=2247069;			
RA	Williams F.E., Trumbly R.J.;			
RT	"Characterization of Tup1, a mediator of glucose repression in			
RT	Saccharomyces cerevisiae.";			
RL	Mol. Cell. Biol. 10:6500-6511(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91153643; Pubmed=1900249;			
RA	Zhang M., Rosenblum-Vos L.S., Lowry C.V., Boake K., Zlotner R.S.;			
RT	"Cloning of the yeast SFL2 gene: its disruption results in			
RT	involved in control of heme-regulated and catabolite-repressed			
RT	genes.";			
RL	Gene 97:153-161(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DBY747;			
RX	MEDLINE=90322611; Pubmed=2197185;			
RA	Fujita A., Matsumoto S., Kuhara S., Misumi Y., Kobayashi H.;			
RT	"Cloning of the yeast SFL2 gene: its disruption results in			
RT	pleiotropic phenotypes characteristic for tup1 mutants.";			
RL	Gene 89:93-99(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Duesterhoeft A., Erdmann D., Hegemann J., Philippsen P.,			
RA	Schweitzer B., Spiegelberg R.;			
RX	Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SIMILARITY TO BETA SUBUNIT OF G-PROTEINS.			
RX	MEDLINE=91192608; Pubmed=1901518;			
RA	Kearsley S.;			
RT	"The SFL2 (TUP1) protein of Saccharomyces cerevisiae contains a			
RT	repeating motif homologous to beta subunits of G proteins.";			
RL	Gene 98:147-148(1991).			
CC	-1- FUNCTION: MAY FUNCTION AS AN ADAPTER OR COFACTOR TO FACILITATE			
CC	THE GENERAL TRANSCRIPTIONAL MACHINERY. SEEMS TO BE REQUIRED FOR			
CC	NORMAL CELL SURFACE ASSEMBLY. INVOLVED IN REPRESSION OF HEME-			
CC	REGULATED AND CATABOLITE RERESSED GENES.			
CC	-1- FUNCTION: MEDIATOR OF GLUCOSE REPRESSION.			
CC	-1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).			
CC	-1- SIMILARITY: BELONGS TO THE TUP1 FAMILY OF WD-REPEAT PROTEINS.			

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DR      EMBL; M35861; AAA34413.1; -
DR      EMBL; M31733; AAA35182.1; -
DR      EMBL; X16365; CAA34411.1; ALT_INIT.
DR      EMBL; X59720; CAA42259.1; -
DR      PIR; A36362; A36362.
DR      PIR; JN0133; JN0133.
DR      PIR; S11169; S11169.
DR      PIR; S19499; S19499.
DR      TRANSFAC; T03686; -.
DR      SGD; S0000680; TOP1.
DR      InterPro; IPR001680; WD40.
DR      Pfam; PF00400; WD40; 7.
DR      PRINTS; PR00320; GPROTEINRPT.
DR      PRODOM; PD000018; WD40; 4.
DR      SMART; SM00320; WD40; 7.
DR      ProSITE; PS00678; WD_REPEATS_1; 4.
DR      ProSITE; PS00082; WD_REPEATS_2; 5.
DR      ProSITE; PS50294; WD_REPEATS_REGION; 1.
KW      Transcription regulation; Repressor; Repeat; WD repeat.
FT      REPEAT          342   371       WD 1.
FT      REPEAT          441   471       WD 2.
FT      REPEAT          483   513       WD 3.
FT      REPEAT          524   553       WD 4.
FT      REPEAT          574   604       WD 5.
FT      REPEAT          628   658       WD 6.
FT      REPEAT          670   706       WD 7.
FT      DOMAIN          97    118       POLY-GLN.
FT      DOMAIN          181   198       POLY-GLN.
FT      DOMAIN          399   409       THR-RICH.
FT      CONFLICT        75     75       E -> A (IN REF. 1).
FT      CONFLICT        100    100      R -> Q (IN REF. 1).
FT      CONFLICT        685     685      P -> S (IN REF. 1 AND 2).
SQ      SEQUENCE        713 AA; 78307 MW; 444104AD63CB944 CRC64;
Query Match           5.8%; Score 108; DB 1; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.24; Indels 46; Gaps 11;
Matches 62; Conservative 30; Mismatches 89;
OY      60 GRPHKPSGTVAVAFRSDDITNOCYOELSERPENCTHRSSVFVGCKYTEYFS----AS 115
DB      86 GRDHQIASLTVOQRQQOQQOQQOQQOQHLLQQQ-QQLAASASAVPAVQAQPATTSATATPAA 144
OY      116 NMLTPRPHPFKLITINRPNDSCMYIVYLRLDDEKEPI-----D 154
DB      145 NMTTSPSAF--PVQASRNVLGS-----QLPTTLIPVRSSVNAQQQLPOQLQQLQOLQQ 197
OY      155 VFAIGLSVAYQFANTATGALGLYSKACRTFGDLTYVOL-EAYLTRESWRMWAYV-----A 208
DB      198 OPPPGVSAPLASNTAING---SPISKETTTLYSVAKAPESTIKETPERENNNTSKIINDTGSA 254
OY      209 TEATTTSAEAT--TPPTVATSASELEAHHTFPMLENGVDHYEPTP 253
DB      255 TTATTTTATEFEIKPKEDATPAS-LHODHYLVYNQR-AHNSKRIP 299
RESULT 9
ID      VGLI_HSV23              STANDARD;             PRT;            372 AA.
AC      P06764;
DT      01-JAN-1988 (Rel. 06, Created)
DT      01-JAN-1988 (Rel. 06, Last sequence update)
DT      01-OCT-1996 (Rel. 34, Last annotation update)
GN      Glycoprotein I.
GE      GI OR US7.
```

OS Herpes simplex virus (type 2 / strain 333).
 OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 ON NCBI_TaxID=10313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86291145; PubMed=3016980;
 RA Hodgman T.C., Mison A.C.;
 RT "The herpes simplex virus type 2 equivalent of the herpes simplex
 RT virus type 1 US7 gene and its flanking sequences.";
 RL Virology 153:1-11(1986).
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GD, GI, AND GE.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
 CC AND TO PRV GP63.
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 CC -----
 CC EMBL: M14886; AAA45861.1;
 CC EMBL: D00026; BA00021.1;
 CC FTR: A05246; Q08E8;
 CC InterPro: IPR002874; Herpes_g1.
 CC Pfam: PF01688; Herpes_g1; 1.
 CC Glycoprotein: 156
 CC CARBOHYD 156
 CC FT CARBOHYD 169
 CC FT CARBOHYD 175
 CC FT CARBOHYD 243
 CC SEQUENCE 372 AA; 39548 MW; B83A9E2D20D8AD3D CRC64;
 SQ
 Query Match 5.78; Score 107; DB 1; Length 372;
 Best Local Similarity 21.08; Pred. No. 0.12;
 Matches 74; Conservative 51; Mismatches 163; Indels 64; Gaps 13;
 OY 3 SLGCTALLAATLAPGAMGIVITGNHVSARIDDDHIVAPREPATIQ-----OLFF 56
 DB 5 SLQG-LAILGLMWC--ATGLVNGPPTVSL-VSDSLVDAGAVGPGFVEDLAVFGELEHF 59
 OY 57 MPOGRPKPYSGTVRAFRSDITNOQYQELSEERFENCTHRSSVFGCKVETYSASN 116
 DB 60 VQAQVPTNYDDIIELEFHYPLGNHCPVAVVTLTACRRPAVAFILCRSTHANS--- 116
 DB 117 RLTGPPHPF-----KLTRNRPNDGMEFYVIRLD--TKEPIDVPAIQLSYQFA 166
 DB 117 ---PAYPTELEGLAQLPLRYRATRDYGLVLRWVGSATNSLFLVALS---A 168
 OY 167 NTAATRGVYKASCRFTGLPTVOLEAVLRTESRMWQAVYVATEATTSAEATTPPVTA 226
 DB 169 NGTFVNGSDYSCDPAQLP-----FSAPRLGPSVYTPGASPTPPT 212
 OY 227 TSASELEAHEFTFPMLENGVDHYEPTPANENSVYRLTMSPTLIGTVAAVSATIGL 286
 DB 213 TTPSPSPDPTPAPG---DIGTPAPASGERAPPNSTASSESHRLTLVAVOIAIPA 267
 OY 287 VIVISIVYTRN-MCTPRKLDIVSODDERSGTRESKRFQ-MVACEINKKA 336
 DB 268 SLIAFVFLGSCICFIHRC-----QRRRRRPGGIYINPGVSCAVNEAA 310
 RESULT 10
 ID VGLI_HSV2H STANDARD; PRT; 372 AA.
 AC P13291;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Glycoprotein I.

GN GI OR US7.
 OS Herpes simplex virus (type 2 / strain H652).
 OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 ON NCBI_TaxID=10315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87111457; PubMed=3027242;
 RA McGeoch D.J., Moss H.W.M., McNab D., Frame M.C.;
 RT "The unique long and unique short unique component of the herpes simplex virus type 2 genome:
 RT identification of the gene encoding glycoprotein G, and evolutionary
 RT comparisons".
 RL J. gen. Virol. 68:19-38(1987).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC RA Dolan A.;
 CC Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GD, GI, AND GE.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
 CC AND TO PRV GP63.
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 CC -----
 CC EMBL: X04798; CA28485.1;
 CC EMBL: Z86099; CAB06714.1;
 CC FTR: F43674; F43674.
 CC InterPro: IPR002874; Herpes_g1.
 CC Pfam: PF01688; Herpes_g1; 1.
 CC Glycoprotein: 156
 CC CARBOHYD 156
 CC FT CARBOHYD 169
 CC FT CARBOHYD 175
 CC FT CARBOHYD 243
 CC SEQUENCE 372 AA; 39558 MW; C0D4A22CAB16B8D7 CRC64;
 SQ
 Query Match 5.38; Score 99; DB 1; Length 372;
 Best Local Similarity 21.08; Pred. No. 0.58;
 Matches 74; Conservative 49; Mismatches 165; Indels 64; Gaps 13;
 OY 3 SLGCTALLAATLAPGAMGIVITGNHVSARIDDDHIVAPREPATIQ-----OLFF 56
 DB 5 SLQG-LAILGLMWC--ATGLVNGPPTVSL-VSDSLVDAGAVGPGFVEDLAVFGELEHF 59
 OY 57 MPOGRPKPYSGTVRAFRSDITNOQYQELSEERFENCTHRSSVFGCKVETYSASN 116
 DB 60 VQAQVPTNYDDIIELEFHYPLGNHCPVAVVTLTACRRPAVAFILCRSTHANS--- 116
 DB 117 RLTGPPHPF-----KLTRNRPNDGMEFYVIRLD--TKEPIDVPAIQLSYQFA 166
 DB 117 ---PAYPTELEGLAQLPLRYRATRDYGLVLRWVGSATNSRFLVALS---A 168
 OY 167 NTAATRGVYKASCRFTGLPTVOLEAVLRTESRMWQAVYVATEATTSAEATTPPVTA 226
 DB 169 NGTFVNGSDYSCDPAQLP-----FSAPRLGPSVYTPGASPTPPT 212
 OY 227 TSASELEAHEFTFPMLENGVDHYEPTPANENSVYRLTMSPTLIGTVAAVSATIGL 286
 DB 213 TTPSPSPDPTPAPG---DIGTPAPASGERAPPNSTASSESHRLTLVAVOIAIPA 267
 OY 287 VIVISIVYTRN-MCTPRKLDIVSODDERSGTRESKRFQ-MVACEINKKA 336
 DB 268 SLIAFVFLGSCICFIHRC-----QRRRRRPGGIYINPGVSCAVNEAA 310
 RESULT 11

[illegible]

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Oy 237 FTFPMLENGVDEHPTPANENSNVTVRLGTMSPTLLIGTV-----AAVVSATITL 286
Db 547 -----VELTE-TPVSLSEPLEVVOLETAVVTETVTVTKANVEPEVLAAVEAPLAV 596

Oy 287 VIVISIVTRNMCTTPRRKLDVTSQDDEERSQTRRESKRFG--PMVACEINKGADODSEL 342
Db 597 EPIVETST-----TLAAETVEEAQVQESNAVAVEPALETESKATSEAOAEL 643

RESULT 12
ID YD76_MYCPN STANDARD: PRF, 1140 AA.
AC P75405;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN376 (A19_0rfl140).
GN MPN376 OR MP460.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreih R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN375.
CC -1- SIMILARITY: IN THE CENTRAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPR374.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
CC MPN373.
CC -----
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CC -----
DR EMBL; AE000045; AAB96108.1; -
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 1098 1118 POTENTIAL.
SQ SEQUENCE 1140 AA; 130383 MW; 8FA9406C57DD8886 CRC64;

Query Match 5.3%; Score 98.5; DB 1; Length 1140;
Best local similarity 20.5%; Pred. No. 2.7; Indels 91; Gaps 15;
Matches 68; Conservative 53; Mismatches 119;

Oy 71 RVAFSDDITNOC-YOELSEERFE-NCTHRSSVFGCKVETXTFASASNLRTGPPHFKLT 128
Db 680 RERPKDINDNIYKVGISIEETIKVAIVKVDMLMARSDPKLAS---VOSTAKKYGLN 736

Oy 129 IR-NRPNDSGMEFYIV-----RLDDTK-----EPIDVFAIQLSVYOPAN-- 167
Db 737 LRSNRY---TQGFVVVVVTVNANDIGNORRANNAASYFYIEGLDKGAOSSYLVEFNQ 793

Oy 168 -----TAMTRGLYSKASCTPGLPVIYQLEAVYRTES-----WRMMQVYVTEATT 213
Db 794 KLYSLESLAVDSRGILYV-----NVSKAIIQAQONOLYLDTHNMN--ALKAWL 842

Oy 214 TSAEATPTPTPVATSGASELEAHEFTFPMLENGVDHDEPTPANENSNVTVRLGTMSPTLLG 273
Db 843 TNAELTLLPT-ASADNSAATLS-----TPNAENE-----GFLSENVSG 878

Oy 274 VTVAAVASATIGLVIVISIVTRNM-----CTPHRKLDVTSQDDEERSQTRRE 320

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Db 879 SLIGYERNTGKFLKERSYENKNNLRLTSLNTLDKNGLEVNDPSVINOYEE 938
 Oy 321 SRKFGPMACETINKGADODSELVELVAIYNP 351
 Db 939 AKGYNYLVESEKGDPSDKNKRITLTNP 969

RESULT 13
 CD44_RAT STANDARD; PRT: 503 AA.
 AC P26051; Q99021; (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 41, Last annotation update)
 DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-1)
 DE Extracellular matrix receptor (ECMR-III) (GP90 lymphocyte
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
 DE (LY-24).
 CD44.
 CC Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID-10116;
 RN 111
 RA SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX STRAIN-BDIX; ISSUO-Pancreas;
 RX MEDLINE-91191532; PubMed-1707342;
 RA Hausmann U., Holmann M., Rudy W., Reber S., Zoeller M.,
 RA Hausmann I., Matzku S., Wenzel A., Ponta H., Herrlich P.:
 RA "A new variant of glycoprotein CD44 confers metastatic potential to
 RA rat carcinoma cells.";
 RA Cell 65:13-24(1991).
 RL 121
 RN SEQUENCE FROM N.A. (ISOFORMS 1).
 RA Stevens J.W., Miquera R.J.;
 RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAIN CELL SURFACE RECEPTOR FOR HYALURONATE. ADHESION TO
 CC MUCCOSAL HIGH ENDOTHELIAL VENULE AND TO TYPES I AND VI COLLAGEN.
 CC PROBABLY INVOLVED IN MATRIX ADHESION, LYMPHOCYTE ACTIVATION AND
 CC LYMPH NODE HOMING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms: 1/short form and 2/long
 CC form/meta-1 (shown here); are produced by alternative splicing.
 CC -1- PTM: EXTENSIVELY MODIFIED INCLUDING N- AND O-LINKED GLYCOSYLATION,
 CC ADDITION OF THE GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, OF SULFATE,
 CC OR PHOSPHATE TO CYTOPLASMIC DOMAIN SERINE RESIDUES.
 CC -1- SIMILARITY: CONTAINS 1 LINK DOMAIN.
 CC -----
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 CC -----
 CC EMBL; M61875; AAA53532.1; -;
 CC EMBL; M61874; AAA53534.1; -;
 CC EMBL; U52179; AAA97915.1; -;
 CC EMBL; U46957; AAA92920.1; -;
 CC HSSP; P98066; ITSG.
 CC InterPro; IPR001231; CD44_antigen.
 CC InterPro; IPR00538; Link.
 CC Pfam; PF00193; Xlink; 1.
 CC PRINTS; PR00658; CD44.
 CC PRODOM; PD000918; Link; 1.
 CC SMART; SM00445; Link; 1.
 CC PROSITE; PS01241; Link; 1.
 CC Cell adhesion; Transmembrane; Glycoprotein; Phosphorylation;
 CC Receptor; Proteoglycan; Sulfate; Signal; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 503 CD44 ANTIGEN.

FT DOMAIN 22 410
 FT TRANSMEM 411 431
 FT DOMAIN 432 503
 FT DOMAIN 51 123
 FT MOD_RES 56 122
 FT DISULFID 56 122
 FT DISULFID 80 100
 FT CARBOHYD 28 100
 FT CARBOHYD 60 60
 FT CARBOHYD 103 103
 FT CARBOHYD 114 114
 FT CARBOHYD 124 124
 FT CARBOHYD 266 266
 FT CARBOHYD 274 274
 FT CARBOHYD 306 306
 FT VARSPIC 224 385

CONFLICT 74 74 R -> S (IN REF. 2).
 FT SEQUENCE 503 AA; 55945 MM; FB489D09BD4EE22 CRC64;
 SQ

Query Match 5.3%; Score 98; DB 1; Length 503;
 Best Local Similarity 22.2%; Pred. No. 1;
 Matches 47; Conservative 30; Mismatches 79; Indels 56; Gaps 10;

Oy 178 ASQRTGDLPTVLEAYLRTESW--RNMQ-----AVVATEATTSAETPTPTVT 225
 Db 297 ATSTWADNNTTEEAATQKEKFNEMQCKNPPPSDSHV-TEGTAAAHNNHPSQM 355
 Oy 226 ATNSAELEHHTFPMLNGVDHPE-----TPANESVTVRLCTMSP 269
 Db 356 TTQSQE-----DVSN-----TDFPDLSHPMGQGHOTESKSSQNDGCTTTSPARR 405
 Oy 270 TLIG---VYAAVSNATGLIVISTYRMCPRPHKIDTYSQODEEESRRESKFP 326
 Db 406 PQLPEMLITLALALILVCAVNSKRCQCKKL--VINSNGTVENRPS----- 458
 Oy 327 WVACEIKGADODSELVELVAIYNPSSALSPD 358
 Db 459 ---ELNGEASKSQEVMH---VKNKEPTPD 483

RESULT 14
 YG46_YEAST STANDARD; PRT: 507 AA.
 AC P53301;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 52.8 kDa protein in BUB1-HIP1 intergenic region.
 GN YGR189C OR G7553.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC NCBI_TaxID-4932;
 RN 111
 RA SEQUENCE FROM N.A.
 RX STRAIN-S280C;
 RX MEDLINE-91279231; PubMed-9133739;
 RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
 RA Nombela C.;
 RT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
 RT of Saccharomyces cerevisiae chromosome VIII."
 RL Yeast 13:357-363(1997).
 CC -1- SIMILARITY: SOME, TO YEAST UTR2.
 CC -----
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DR EMBL: 272974; CAA97215.1; -
 DR EMBL: X99074; CAA67525.1; -
 DR HSSP: P23904; IAKR.
 DR SGD: S0003421; CRH1.
 DR InterPro: IPR000757; Glyco_hydro_16.
 DR Pfam: PF00722; Glyco_hydro_16; 1.
 KW Hypothetical protein.
 FT DOMAIN 63 66 POLY-SER.
 FT 301 310 POLY-SER.
 FT 345 357 POLY-SER.
 FT 387 391 POLY-SER.
 FT DOMAIN 467 470 POLY-SER.
 SO SEQUENCE 507 AA; 52757 MW; 7D7B61F57AE942C CRC64;

Query Match 5.3%; Score 98; DB 1; Length 507;
 Best Local Similarity 21.7%; Pred. No. 1.1;
 Matches 54; Conservative 46; Mismatches 95; Indels 54; Gaps 9;

136 DSMFVIVYRLDDTKPEIDVFALQLSVQFANTATRGLYSKASCTFGLPTVQLAYLR 195
 278 DGGSIY--GRYDQAEDEFAVLANGSISSTSVSSASTSVSSVSSSTSSSSAST 335
 196 TEESMRNMAVYATETTTSAEATPTPTVATSELEAEHFTFPLENGVDHFEPTPAN 255
 336 VSSS---VSTVSSSSSVSSSTSPSSSTATSKTLASSVT---TSSSISFE-KOSS 388
 256 ENSNVVRCLTMSPTLIGYV-VAAYVSATIGLYIVISYTRNCTPHRLKIDVVSOD--- 310
 389 SSSSKTKVASTSTSESIISSTKPTATVSSST-----TRSTVAPPTQOOSVSSDSPVO 438
 311 -----DEERSQTRRESKRFPMV-----ACEIKKGADQ-----S 340
 439 DRGCVATSSNDVTSSTTQISSKTTITQSSSEASTNSVOISNGADLAOSLPREGKLP 498
 341 ELVELVAIV 349
 499 VLVALLALL 507

RESULT 15
 ID SLN1_YEAST STANDARD; PRT: 1220 AA.
 SLN1_YEAST
 AC P39928;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 OS Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
 GN SLN1 OR YPD2 OR YIL147C.
 GN Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C / AB972;
 RA Churchill B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Genies S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones A.,
 RA Louis E., Lye G., Moule S., O'Neill C., O'Neill C., Pearson D.,
 RA Rajendram M.A., Riles L., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP MUTAGENESIS OF HIS-576 AND ASP-1144.
 RX MEDLINE-94239498; PubMed-8183345;
 RA Maeda T., Wurgler-Murphy S.M., Saito H.;
 RT "A two-component system that regulates an osmosensing Map kinase
 RT cascade in yeast.";
 RL Nature 369:242-245(1994).
 CC -1- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 CC SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
 CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SKS2/SSK2->
 CC PBS2->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
 CC PROTEIN TO ACTIVATE SSK2 AND SSK2, TWO MARKERS THAT FURTHER
 CC STIMULATE THE PBS2-HOG1 MARK CASCADE. IN LOW OSMOLARITY MEDIA,
 CC THE ACTIVATED SLN1 HISTIDINE KINASE REPRESENTS THE ACTIVATION OF THE
 CC PBS2-HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
 CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC -----
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DR EMBL: 238059; CAA86131.1; -
 DR EMBL: 001835; AAC48912.1; -
 DR PIR: S48888; S48888.
 DR PIR: S48387; S48387.
 DR HSSP: P06143; IUDR.
 DR SGD: S0001409; SLN1.
 DR InterPro: IPR003594; AtPbind_AtPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR InterPro: IPR003661; His_Kina.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00072; response_reg; 1.
 DR Pfam: PF00512; signal; 1.
 DR Pfam: PF02518; HATPase_C; 1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR ProDom: PD000039; Response_reg; 1.
 DR SMART: SM00387; HATPase_C; 1.
 DR SMART: SM00388; HSKA; 1.
 DR SMART: SM00448; REC; 1.
 DR PROSITE: PS50109; HIS_KIN; 1.
 DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
 DR Sensory transduction; Transferase; Kinase; Phosphorylation;
 KW Transmembrane.
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT DOMAIN 47 333
 FT TRANSMEM 334 354
 FT DOMAIN 355 1220
 FT DOMAIN 573 928
 FT DOMAIN 1089 1210
 FT MOD_RES 576 576
 FT MOD_RES 1144 1144
 FT CARBOHYD 100 100
 FT CARBOHYD 138 138
 FT CARBOHYD 142 142
 FT CARBOHYD 181 181
 FT CARBOHYD 224 224
 FT CARBOHYD 272 272
 FT MUTAGEN 576 576
 FT MUTAGEN 891 891
 FT MUTAGEN 1144 1144
 SO SEQUENCE 1220 AA; 134434 MW; 45FEE24A8165486B CRC64;

Tue May 6 18:37:35 2003

us-09-993-777-68.rsp

Page 11

Query Match	5.28;	Score 97;	DB 1;	Length 1220;
Best Local Similarity	22.7%;	Pred. No. 4;		
Matches	58;	Conservative	43;	Mismatches 104;
			Indels	50;
			Gaps	11;

[illegible]

Search completed: May 5, 2003, 16:13:39
Job time : 17.5 secs

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:08:23 ; Search time 28 seconds

(without alignments)
2663.895 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1863

Sequence: 1 MASLIGTIALAATLAPFGA.....VELVAIVNPSALSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:
2: SP_BACTERIA:
3: SP_FUNGI:
4: SP_HUMAN:
5: SP_INVERTEBRATE:
6: SP_MAMMAL:
7: SP_MHC:
8: SP_ORGANELLE:
9: SP_PLANT:
10: SP_RODENT:
11: SP_VIRUS:
12: SP_VIRUS:
13: SP_VIRUS:
14: SP_VIRUS:
15: SP_VIRUS:
16: SP_VIRUS:
17: SP_VIRUS:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	12	Q67645 gallid herp
2	164	8.8	420	12	Q39309 equine herp
3	162.5	8.7	354	12	Q98VNI human herp
4	158	8.5	420	12	O55525 equine herp
5	156	8.4	384	12	O69357 feline herp
6	154	8.3	384	12	O69331 feline herp
7	152	8.2	355	12	Q96E15 turkey herp
8	149	8.0	355	12	Q69287 turkey herp
9	148	7.9	364	12	Q9YPA1 canine herp
10	147	7.9	364	12	O41525 canine herp
11	147	7.9	359	12	O91335 canine herp
12	145	7.8	370	12	O86789 phocid herp
13	140.5	7.5	369	12	O91E39 bovine herp
14	139.5	7.5	382	12	O39505 pseudocarb
15	130.5	7.0	366	12	O99F67 turkey herp
16	125	6.7	356	12	Q88524 turkey herp

17	124.5	6.7	683	12	Q36401 alicetaphine
18	123	6.6	355	12	Q67638 gallid herp
19	115	6.2	433	11	O55054 mus musculu
20	115	6.2	457	11	Q61396 mus musculu
21	108.5	5.8	319	5	Q9W357 drosophila
22	106.5	5.7	235	5	Q9YV19 drosophila
23	103	5.5	982	12	O9VIG1 drosophila
24	102.5	5.5	378	4	O9W415 drosophila
25	102.5	5.5	4498	5	O9W223 drosophila
26	99	5.3	279	5	O9U474 caenorhabdi
27	97.5	5.3	1011	5	O9NH29 helicoverpa
28	97.5	5.2	1714	5	O9W1X4 drosophila
29	96.5	5.2	814	13	O91897 xenopus lae
30	96	5.2	877	4	O9H306 homo sapien
31	96	5.2	878	4	O9H307 homo sapien
32	96	5.2	957	4	O14651 homo sapien
33	96	5.2	1217	4	O9UKW9 homo sapien
34	95.5	5.1	332	12	O8V0L9 equine herp
35	95.5	5.1	337	12	O8V0M1 equine herp
36	95.5	5.1	342	12	O8V0L8 equine herp
37	95.5	5.1	356	12	O8V0L7 equine herp
38	95.5	5.1	357	12	O8V0M2 equine herp
39	95.5	5.1	372	12	O8V0M3 equine herp
40	95.5	5.1	374	12	O8V0L6 equine herp
41	95.5	5.1	389	12	O8V0M0 equine herp
42	95.5	5.1	826	12	O8V0L5 equine herp
43	95.5	5.1	867	12	O39782 equine herp
44	95	5.1	745	5	O9VYJ9 drosophila
45	95	5.1	1844	5	Q22579 caenorhabdi

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	362 AA.
ID	Q67645		
AC	Q67645		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	Glycoprotein I.		
OS	Gallid herpesvirus 1.		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.		
OX	NCBI_TaxID=10386;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-USDA CHALLENGE STRAIN:		
RX	MEDLINE=9703380; PubMed=8879127;		
RA	Wild M.A., Cook S., Cochran M.;		
RT	"A genomic map of infectious laryngotracheitis virus and the sequence and organization of genes present in the unique short and flanking regions."		
RL	Virus Genes 12:107-116(1996).		
DR	EMBL; U28832; AAC5101.1; -		
DR	InterPro; IPR002874; Herpes_g1.		
DR	Pfam; PF01688; Herpes_g1; 1.		
SO	SEQUENCE 362 AA; 39750 MW; F530C1A7CC6BA5 CRC64;		
Query Match	100.0%; Score 1863; DB 12; Length 362;		
Best Local Similarity	100.0%; Pred. NO. 1.3e-160;		
Matches 362; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MASLIGTIALAATLAPFGANGIVITGNHVSARIDDDHIVIAAPPETIQLQFFPQ 60		
DB	1 MASLIGTIALAATLAPFGANGIVITGNHVSARIDDDHIVIAAPPETIQLQFFPQ 60		
QY	1 RPHKPSGVRAVAFNSDITNOCYELSEERENCTHRSSVVGCKVTEYFSSNRLTG 120		
DB	1 RPHKPSGVRAVAFNSDITNOCYELSEERENCTHRSSVVGCKVTEYFSSNRLTG 120		
QY	121 PPHFKLTIRNPNDSGTFYIVRLDQTEKPIIDVAQLSLVYQPNANATRGITSNAS 180		

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Db 121 PPHFKLTINRPNDGMYIVRLDDTKEPDIQVFAIQLSVQFANTATRGYSKASC 180
QY 181 RTFCLPTVQLEAVLRTESNRNMQAYVATATTSAEATPTPTATTSASELEHFTFP 240
Db 181 RTFCLPTVQLEAVLRTESNRNMQAYVATATTSAEATPTPTATTSASELEHFTFP 240
QY 241 WLENGVDHYEPTPANENSNTVRLGTWSPTLIGVTAAVVSATIGLVISIVTRNCTP 300
Db 241 WLENGVDHYEPTPANENSNTVRLGTWSPTLIGVTAAVVSATIGLVISIVTRNCTP 300
QY 301 HRKLDVTSQDDERSQTRRESRKGPVACEINKGADQDSEVELVAIVPSSALSPDSI 360
Db 301 HRKLDVTSQDDERSQTRRESRKGPVACEINKGADQDSEVELVAIVPSSALSPDSI 360
QY 361 KM 362
Db 361 KM 362

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RESULT 2

039309 PRELIMINARY; PRT; 420 AA.

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AC 039309:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Counterpart of HSV-1 gene US7 and VZV gene 67.
GN 73.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RX MEDLINE=98264497; PubMed=9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4."
RL J. Gen. Virol. 79:1197-1203(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RX Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030027; AAC59593.1;
DR InterPro; IPR002874; Herpes_g1.
DR Pfam; PF01688; Herpes_g1.1.
SQ SEQUENCE 420 AA; 45710 MW; 1EB944825DF3D852 CRC64;

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Query Match 8.8%; Score 164; DB 12; Length 420;
 Best Local Similarity 25.5%; Pred. NO. 1.8e-06;
 Matches 96; Conservative 50; Mismatches 143; Indels 88; Gaps 21;

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QY 10 LLAATLAPFGAMGIVTGNHVSARIDDDHVIYAPREAIQL-QLEFMGQR-PHPRYS 67
Db 13 LLAISMCK---ATAIYRGHSMYLNASSFPAYPKDKSLVVVGHMFLDGOQLPTTNY 69
QY 68 GTVAFAFRSDITNOCYOELSEERENCTHRSSVFVGC--KTEYTPSASNRLTGPHPF 125
Db 70 GLEEL-IHHYISRGCVIVITISIESCPRYANNAFRSCLIKTSHNDYTHVNTSVETNV 128
QY 126 KLTIRNRPNDGMYIVRLDDTKEPDIQVFAIQLSVYOF-ANTAAATRGYSKASCRTFG 184
Db 129 LLAITRPOPADSGAYILRVKLHNA-PTADVGSFAFYDLSQNTVPEPPTAKEPSNVFT 187
QY 185 LPTVQLEAVLRTESNRNMQAYVATATTSAEATPTPTATTSASELEHFTFP 241
Db 188 RTAPAPANTSTK-----TGSNTTSSOSTWLTLPPTP-----RPA 221
QY 242 LKNGVDHYEPTPANEN--SNVTVRL-----GTMSPT-----LIGVTAAVVSATIG-- 285
Db 222 LEL---LITAPANEVYSQDTAMLCGHRPSTAVPTIYHMLGLT-----GNLPE 269

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QY 286 --LVIVISIVTRNCTP-HRKLDVTS-----QDDERSQTRRESR-KRGPV---ACEIN 333
Db 270 DVLIEDSEILR---RPPRPQQTSSRTEDGDKQNTSTSPKSRNKIVANVVIPTACVLM 326
QY 334 KGADQDSEVELVAIVN 350
Db 327 -----LLLVVGAIIIN 337

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RESULT 3

098VN1 PRELIMINARY; PRT; 354 AA.

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AC 098VN1:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE ORF67.
OS Human herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=10335;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RX MEDLINE=21109116; PubMed=11162813;
RA Faga B., Maury W., Bruckner D.A., Grose C.;
RT "Identification and Mapping of Single Nucleotide Polymorphisms in the Varicella-zoster Virus Genome."
RL Virology 280:1-6(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RA Cole N.L., Faga B.P., Grose C.;
RX Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-VIA;
RA Grose C., Faga B.;
RT "Identification and mapping of single nucleotide polymorphisms in the varicella-zoster virus genome."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF314221; AAK19249.1;
DR EMBL; AF325441; AAK01055.1;
DR InterPro; IPR002874; Herpes_g1.
DR Pfam; PF01688; Herpes_g1.1.
SQ SEQUENCE 354 AA; 39373 MW; 3F01739F3AFC6B08 CRC64;

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Query Match 8.7%; Score 162.5; DB 12; Length 354;
 Best Local Similarity 22.4%; Pred. No. 2e-06;
 Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

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QY 23 IVTGNHVSARIDDDHVIYAPRE--ATIQLEFMGQR-HRPSGVAFARSDI-78
Db 21 LIRKGDHVSQVASSLSLILIPQNDNYTEIKQVLFISQLRTGYNISSTLELL-ADT 79
QY 79 TNOCYOELSEERENCTHRSSVFVGCYV--EYTFASNRLTGPHPKLTIRNRPN 135
Db 80 VACCPFSVQVIRVDCPRIRTSAFISCRYKSHWYGNSTDRISTEPDAGVMLKITYRGIN 139
QY 136 DSGMFYIVRLDDTKEPDIQVFAIQLSVY-----QTAAPATRGYSKAS 179
Db 140 DAGVVYVLLVRLDHSRS-TDGFILGVNVYTAGSHNHIGVLYTSPSLQNGYSTALFOQA- 197
QY 180 CRTFGILPT-----VQLEAVLRTES--WRNMQAYVATATTSAEATPTPT 225
Db 198 -RLCDLPATPKGSGTSLPQMLDLRAGKSLIEDPMLH-EDVYTTETKSVYKKG----- 248
QY 226 ATASELEHFTFPWLENGVDHYEPTPAN--ENS-----NVTVRLGTMSPTLIGVTV 276
Db 249 -----IEN---HVYPTDMSTLPEKSLNDPEKLL-----IIPYA 281
QY 277 AAVVSATIGLVISIVTRNM 297

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SQ SEQUENCE 384 AA; 43019 MW; C9ACE129E496DC1 CRC64;
 Query Match 8.3%; Score 154; DB 12; Length 384;
 Best Local Similarity 22.3%; Pred. No. 1.3e-05;
 Matches 73; Conservative 52; Mismatches 133; Indels 70; Gaps 13;
 OY 5 LGTLLAALTAAPFGMGVITTSNHSARIDDDHIYVAPRE-ATIQLOLFMPGQ-RP 62
 DB 1 MSSIAIYITLMAIGTVYGVYRGDHSVLHVDSSGFEVITPLENFIYGLILFDQPLP 60
 OY 63 HKVSGTVARAFSDITNOCYSELSERFENCRHSSSVFVC--KYTEXTFSANRLTG 120
 DB 61 VNNYNQTLF-IHYNHSSCYKIVQYIEYSSCRVANNMFRSCLAKHTSMHQYQLSINTS 119
 OY 121 PPHFRLTIRNPRNDSCGFYIVRLDQTKEPIDFAIQLSVYQFANTAATRLYSKASC 180
 DB 120 VETGMLLTITSPKMDGGIYALRVRENHNK-ADVFGLSVFYSF---DTRGHRHHADE 174
 OY 181 RTFG--LPYVO-LEAYLRTEESRNNOAY---VATEATTSAAATPTPTVATASAELEA 234
 DB 175 NLNGELITPPSPMETYVKV---NTPYDHVYTTQTTSKMSSEPSNTSISC----- 223
 OY 235 EHFTFPMLENGVDHYEPTPANENSNTVRL-----GTMSPTLIGTVAA 278
 DB 224 -----HTFONDPNEGETLYTHLNTAGNITTDMDVMDGTTLAFRLIDGKLN 270
 OY 279 VVSAT-----IGLVIVISI 292
 DB 271 SVTSSFKNETTQKWTDRKGVFVVISI 298
 RESULT 7
 OY 09E6L5 PRELIMINARY; PRT; 355 AA.
 AC 09E6L5;
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE US7 membrane glycoprotein I-like protein.
 GN MDV095.
 OS Turkey herpesvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OX NCBI_TaxId=10390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=MD5;
 RC MEDLINE=20392152; PubMed=10933706;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.:
 "The genome of a very virulent Marek's disease virus."
 J. Virol. 74:7980-7988 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MD5;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.:
 Submitted (MAR-2000) to the EMBL/Genbank/DBD databases.
 RL EMBL; AF243438; AAG14269.1;
 DR InterPro: IPR002874; Herpes_g1.
 DR Pfam: PF01688; Herpes_g1.
 SQ SEQUENCE 355 AA; 40568 MW; D23A6DA126ACDB00 CRC64;
 Query Match 8.2%; Score 152; DB 12; Length 355;
 Best Local Similarity 22.9%; Pred. No. 1.8e-05;
 Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;

OY 135 NDSGMFYIVRLDQTKEPIDFAIQLSVYQFANTAATRLYSKASCRTGLPTVQLEAYL 194
 DB 132 SDTGSYIRVALAG-RNMSDIFRMAVIRS-----SKSMCNHSSASFQHKCI 179
 OY 195 RTEE--SWRMQAVVATEATTSAEATTPPVATASAELEAHFEPMLENGVDHYEPT 252
 DB 180 RYVDRAAFENYLLIGHVGNLSDSELHAIVNITPOST-TDNIITTPFDNSGTTISPT 238
 OY 253 P--ANENSNTVRLGT-MSPTLIGTVAAV--SATIGLVI---ISIVRNKCTPHRK 303
 DB 239 VFNLFNNSHVDAMNSTMGMNTVLYKTLPRLIYFSMIVLCIALAIYLCERCSPHR 298
 OY 304 LDTVSODDERSCOTRRBSKRGPMVACEIKKGADQSEIVE 344
 DB 299 I---YIGEPKRSDE-----APLITSAVNESFOYDYNVKE 328
 RESULT 8
 OY 069287 PRELIMINARY; PRT; 355 AA.
 AC 069287;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE Membrane glycoprotein I precursor.
 GN US7.
 OS Turkey herpesvirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OX NCBI_TaxId=10390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95133166; PubMed=7831788;
 RA Brunovskis P., Velicer L.F.:
 "The Marek's disease virus (MDV) unique short region:
 alphaherpesvirus-homologous, fowlpox virus-homologous, and MDV-
 specific genes."
 J. Virol. 206:324-338 (1995).
 RL EMBL; I22174; AAA64968.1;
 DR InterPro: IPR002874; Herpes_g1.
 DR Pfam: PF01688; Herpes_g1.
 KW Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 355
 FT SEQUENCE 355 AA; 40579 MW; 40CD25034E4EAE6F CRC64;
 Query Match 8.0%; Score 149; DB 12; Length 355;
 Best Local Similarity 23.3%; Pred. No. 3.3e-05;
 Matches 80; Conservative 54; Mismatches 163; Indels 46; Gaps 15;
 OY 19 GAMGIYITGNHSARIDDDHIYVAPR--PEATIQLOLFMPGQRPKPYSGTVARAFR 75
 DB 15 GIMSIYVTGTSTV--LSTQDSALVAFRGDKMKNVVGQLFLDQTRTSYTGTTET-LK 71
 OY 76 SDITNOCYSELSERFENCRHSSSVFVGCKYETFFSANKLITGPPHPK---LITRNP 132
 DB 72 WBEYKCYSLAHTSYMDCPALDATTVRGCRDAVVYAQPGRV--QPFPEKGTLLRIIVE 129
 OY 133 RPNDSGMFYIVRLDQTKEPIDFAIQLSVYQFANTAATRLYSKASCRTGLPTVQLEA 192
 DB 130 RVSDTGSYIRVSLAG-RNMSDIFRMAVIRS-----SKSMCHHSSASFQAHK 177
 OY 193 YLRTEE--SWRMQAVVATEATTSAEATTPPVATASAELEAHFEPMLENGVDHYE 250
 DB 178 CIRYVDRAAFENYLLIGHVGNLSDSELHAIVNITPOST-TDNIITTPFDNSGTTIS 236
 OY 251 PTP--ANENSNTVRLGT-MSPTLIGTVAAV--SATIGLVI---ISIVRNKCTPH 301
 DB 237 PTVFNLFNNSHVDAMNSTMGMNTVLYKTLPRLIYFSMIVLCIALAIYLCERCSPH 296
 OY 302 RKLDVTASODEDEERSCOTRRBSKRGPMVACEIKKGADQSEIVE 344
 DB 297 RRI---YIGEPKRSDE-----APLITSAVNESFOYDYNVKE 328


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DB 133 IENGVLLEITNRPNDGVYFTRVLENNK--TDVFGIDAFIYSF 175
RESULT 12
ID 086789 PRELIMINARY: PRT: 370 AA.
AC 086789;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein 1.
OS Feline herpesvirus (Feld herpesvirus 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirinae.
OX NCBI_TaxID=10334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94267406; PubMed=8207390;
RA Spatz S.J., Rota P.A., Maes R.K.;
"Identification of the feline herpesvirus type 1 (FHV-1) genes
encoding glycoproteins G, D, I and E: expression of FHV-1 glycoprotein
D in vaccinia and raccoon poxviruses."
RL J. Gen. Virol. 75:1235-1244(1994).
DR EMBL, S72415; AAB30901.1;
DR InterPro: IPR002874; Herpes_g1;
DR Pfam: PF01688; Herpes_g1;
SQ SEQUENCE 370 AA; 41568 MW; 2A816ECB37466A77 CRC64;

Query Match
Best Local Similarity 22.0%; Score 145; DB 12; Length 370;
Matches 72; Conservative 52; Mismatches 136; Indels 66; Gaps 14;

DB 124 LCTLLAATLAPFGAGIVITGNHVSARIDDDHIYVAPRE-ATIQOLFEMPQO-RP 62
DB 1 MSIAFIYILMAGIVYIGDGHSLHVDSSGFVITPLENTIYHLFLDQRLP 60
DB 63 HRPSTGVAVARSDITNOCYOLSEERENCCTHSSSVFVGC--KVETYSASRLTG 120
DB 61 VNNYGTLEI-THYHNSHCYKIVQIEYSCPRVNNAFRSCILKHTSMHOYDLSINTS 119
DB 121 PPHPLITRNRPNDGMEFYIVRLDTPKEPIDVFAIOLSVOPANTATGLYSKASC 180
DB 120 VETGMLITTPSKMEDGILALVRPNHNNK-ADVFGLSVFYSF---DFRHRHAE 174
DB 181 RTFG--LPTVQ-LEAVLRTESRMWQAY--VATEATTTSAETTPPTVATASLEA 234
DB 175 NUNGELITTPSPMEYVKV----NTPYIDHWYTTQTSTNKSMSSEPSNTSISC----- 223
DB 235 EHFPTPWLNGVDHYEPTANENSNTVRL-----GIMSPLIGVTVA 278
DB 224 -----HTFQNDPNEGELTYLTLNAGNITYDDVMMDGTLKPRLI----- 264
DB 279 VVSATIGLIVISIVTRNCTPHRKLDT 306
DB 265 -----DMGLNLVTSSEFKN--GNHAKMDT 286

RESULT 13
ID 091E39 PRELIMINARY: PRT: 369 AA.
AC 091E39;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Glycoprotein 1.
OS Phocid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirinae.
OX NCBI_TaxID=47418;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-PB84;
RA Martina B., Osterhaus A.D.M.E., Harder T.C.;
RT "Identification and analysis of immunogenicity of the glycoprotein D
RT equivalent within the unique short segment of phocid herpesvirus-1."
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ290955; CAC51466.1;
DR InterPro: IPR002874; Herpes_g1;
DR Pfam: PF01688; Herpes_g1;
SQ SEQUENCE 369 AA; 42372 MW; 1587181704A7A8A CRC64;

Query Match
Best Local Similarity 25.1%; Score 140.5; DB 12; Length 369;
Matches 57; Conservative 36; Mismatches 89; Indels 45; Gaps 10;

DB 22 GIYITGNHVSARIDDDHIYVAPRE-EATIQOLFEMPQO-R-PPKPSGTVRVAFRSDIT 79
DB 16 GYVRGTVMGMVNTSSGTVVPPDDDFVNTGLFLDQRLPVTNYSGTIEIT--FN 72
DB 80 NCOYOLSEERENCCTHSSSVFVGC--KVETYSASA-----SNRLTGPPIPKLITRNPR 133
DB 73 YCYTYVQTEYVSCPRINNAFRSCLIKYSKHQSLRINSIEFG---VLEIKNPK 128
DB 134 PNDGMEFYIVRLDTPKEPIDVFAIOLSVOPANTATGLYSKASCRTFGLPTVQLEAV 193
DB 129 PSDSGVITFRVLENNK--TDVFGISAIFYSEKSG--ENITKPDSONT----- 173
DB 194 LRTEESRMWQAYVATEATTTSAEA-----TTPPTVATASLEL 232
DB 174 -----ENFTNHLVTPSTTIKPRESESHLNTFPPTDIPAPCHEV 213

RESULT 14
ID 039505 PRELIMINARY: PRT: 382 AA.
AC 039505;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycoprotein 1.
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirinae.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JURA;
RA Goltz M., Buhk H.J., Broil H., Lewin M., Mankertz A., Boernar B.,
RA Borchers K., Weigelt W.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 372-382 FROM N.A.
RC STRAIN-JURA;
RA Schwyzer M.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-JURA;
RA Schwyzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J.,
RA Lowery D.E., Simard C., Bello L.J., Thiry E., Vlcek C.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-COOPER;
RA Goltz M., Buhk H.J., Schwyzer M.;
RT "Nucleotide sequence of the HindIII O and K fragments located in the
RT US region of the bovine herpesvirus 1 genome."
RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ004801; CAA06146.1;
DR EMBL: Z98199; CAB10890.1;
DR InterPro: IPR002874; Herpes_g1;
DR Pfam: PF01688; Herpes_g1;
SQ SEQUENCE 382 AA; 39536 MW; 0F06C95CD2581EC2 CRC64;

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GenCore version 5.1.4-ps-4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:14:43 ; Search time 16.5 Seconds
(Without alignments)
1893.078 Million cell updates/sec

Title: US-09-993-777-68
Perfect score: 1663
Sequence: 1 MASLLGTLALTAATAPGCA.....VELVALVNPASALSPDSIKM 362

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 328255 seqs, 86286685 residues
Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published.Applications.AA.*
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3: /cgn2_6/p/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/p/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/p/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/p/ptodata/2/pubpaa/PCRUS_PUBCOMB.pep.*
8: /cgn2_6/p/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/p/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1863	100.0	362	US-09-881-457A-5	Sequence 5, Appl 1
2	148	7.9	364	US-10-156-275-56	Sequence 56, Appl 1
3	115	6.2	612	US-10-125-692-10	Sequence 10, Appl 1
4	112	6.0	387	US-10-114-893-133	Sequence 133, Appl 1
5	108	5.8	713	US-09-801-368-408	Sequence 408, Appl 1
6	102.5	5.5	379	US-09-813-153-138	Sequence 138, Appl 1
7	97	5.2	1220	US-09-801-368-332	Sequence 332, Appl 1
8	93	5.0	320	US-09-738-626-5621	Sequence 5621, Appl 1
9	92.5	5.0	547	US-09-753-436-1	Sequence 1, Appl 1
10	91	4.9	365	US-09-870-759-73	Sequence 73, Appl 1
11	90.5	4.9	359	US-09-978-295A-45	Sequence 45, Appl 1
12	90.5	4.9	359	US-09-978-697-45	Sequence 45, Appl 1
13	90.5	4.9	359	US-09-978-192A-45	Sequence 45, Appl 1
14	90.5	4.9	359	US-09-999-832A-45	Sequence 45, Appl 1
15	90.5	4.9	359	US-09-978-189-45	Sequence 45, Appl 1
16	90.5	4.9	359	US-10-174-590-42	Sequence 42, Appl 1
17	90.5	4.9	359	US-10-176-758-42	Sequence 42, Appl 1
18	90.5	4.9	359	US-10-175-737-42	Sequence 42, Appl 1
19	90.5	4.9	359	US-10-173-706-42	Sequence 42, Appl 1

20	90.5	4.9	359	US-10-175-738-42	Sequence 42, Appl 1
21	90.5	4.9	359	US-10-175-752-42	Sequence 42, Appl 1
22	90.5	4.9	359	US-10-176-482-42	Sequence 42, Appl 1
23	90.5	4.9	359	US-10-176-757-42	Sequence 42, Appl 1
24	90.5	4.9	359	US-10-176-913-42	Sequence 42, Appl 1
25	90.5	4.9	359	US-10-180-557-42	Sequence 42, Appl 1
26	90.5	4.9	359	US-10-180-557-42	Sequence 42, Appl 1
27	90.5	4.9	359	US-10-173-700-42	Sequence 42, Appl 1
28	90.5	4.9	359	US-10-174-572-42	Sequence 42, Appl 1
29	90.5	4.9	359	US-10-174-579-42	Sequence 42, Appl 1
30	90.5	4.9	359	US-10-174-582-42	Sequence 42, Appl 1
31	90.5	4.9	359	US-10-174-588-42	Sequence 42, Appl 1
32	90.5	4.9	359	US-10-175-739-42	Sequence 42, Appl 1
33	90.5	4.9	359	US-10-175-740-42	Sequence 42, Appl 1
34	90.5	4.9	359	US-10-175-743-42	Sequence 42, Appl 1
35	90.5	4.9	359	US-10-176-488-42	Sequence 42, Appl 1
36	90.5	4.9	359	US-10-176-492-42	Sequence 42, Appl 1
37	90.5	4.9	359	US-10-176-747-42	Sequence 42, Appl 1
38	90.5	4.9	359	US-10-176-750-42	Sequence 42, Appl 1
39	90.5	4.9	359	US-10-176-985-42	Sequence 42, Appl 1
40	90.5	4.9	359	US-10-176-987-42	Sequence 42, Appl 1
41	90.5	4.9	359	US-10-176-991-42	Sequence 42, Appl 1
42	90.5	4.9	359	US-10-176-992-42	Sequence 42, Appl 1
43	90.5	4.9	359	US-10-176-993-42	Sequence 42, Appl 1
44	90.5	4.9	359	US-10-184-658-42	Sequence 42, Appl 1
45	90.5	4.9	359	US-10-173-695-42	Sequence 42, Appl 1

ALIGNMENTS

RESULT 1
US-09-881-457A-5
Sequence 5, Application US/09881457A
Patent No. US20020081316A1
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Cook, Stephanie M
TITLE OF INVENTION: NO. US20020081316A1 Avian Herpes Virus and Uses Thereof
FILE REFERENCE: SY0110510KOK
CURRENT FILING DATE: US/09/881,457A
PRIOR APPLICATION NUMBER: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/426,352
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/804,372
PRIOR FILING DATE: 1997-02-21
PRIOR APPLICATION NUMBER: PCT/US95/10245
PRIOR FILING DATE: 1995-08-09
PRIOR APPLICATION NUMBER: 08/663,566
PRIOR FILING DATE: 1996-06-13
PRIOR APPLICATION NUMBER: 08/288,065
PRIOR FILING DATE: 1994-08-09
PRIOR APPLICATION NUMBER: PCT/US93/05681
PRIOR FILING DATE: 1993-06-14
PRIOR APPLICATION NUMBER: 08/023,610
PRIOR FILING DATE: 1993-02-26
PRIOR APPLICATION NUMBER: 07/898,087
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 362
TYPE: PRT
ORGANISM: Infectious Laryngotracheitis Virus
US-09-881-457A-5
Query Match 100.0% Score 1863; DB 10; Length 362;
Best Local Similarity 100.0%; Pctd. No. 5; Seq-Id 16;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MASLLGTLALTAATAPGACGIVTGNHNSARIDDDHIYVAPPEATLOLOLFEMPG 60
|||||

Db 1 MASLCTALLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPAITQLOLFPMQ 60
Oy 61 RPKRPSGVTVRAFRSDITNOCYOELSEERFENCSTRSSSVFGCKVTETFSASRLTG 120
Db 61 RPKRPSGVTVRAFRSDITNOCYOELSEERFENCSTRSSSVFGCKVTETFSASRLTG 120
Oy 121 PPHFPLTIRNPPNDSGMFYIVRLDTPKEPIDVAIQLSYQFANTATRLYSKASC 180
Db 121 PPHFPLTIRNPPNDSGMFYIVRLDTPKEPIDVAIQLSYQFANTATRLYSKASC 180
Oy 181 RTGGLTVOLEALRTESWRNQAIVATATTSSEATPTPVATSSASELAEHTTP 240
Db 181 RTGGLTVOLEALRTESWRNQAIVATATTSSEATPTPVATSSASELAEHTTP 240
Oy 241 WLENGVDHTEPPRANNSVTVRLGTMSPPLIGTVAAVVSATIGLVIVISYTRMCKTP 300
Db 241 WLENGVDHTEPPRANNSVTVRLGTMSPPLIGTVAAVVSATIGLVIVISYTRMCKTP 300
Oy 301 HRKLDVVSODDERSTRESKRFQPMVACEIKKGADDOSELVELVAIYNPSALSSPDSI 360
Db 301 HRKLDVVSODDERSTRESKRFQPMVACEIKKGADDOSELVELVAIYNPSALSSPDSI 360
Oy 361 KM 362
Db 361 KM 362

RESULT 2
US-10-156-275-56
Sequence 56, Application US/10156275
Publication No. US20030049844A1
GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/156,275
FILING DATE: 28-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/399,118
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-156-275-56

Query Match 7.9%; Score 148; DB 9; Length 364;
Best Local Similarity 27.3%; Pred. No. 16-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

Oy 4 LGCTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPAITQLOLFPMQ 60
Db 16 LITMFLPLIFLFLYGVNGVYKGYTISMFLNLSGFSIFPDCKITVSGSLDLOHUS 75
Oy 63 HKRPSGVTVRAFRSDITNOCYOELSEERFENCSTRSSSVFGCKVTETFSASRLTG 120
Db 76 VNNVSGTIERI---HNNSGYTVQOTIEYFSCRIINMNFRCGLKRVSKHNEQLINNS 132
Oy 121 PPHFPLTIRNPPNDSGMFYIVRLDTPKEPIDVAIQLSYQF 165
Db 133 IENGVLLEITNPKRNDSGVYFIRVLENNK--TDVEGIDAFIVSF 175

RESULT 3
US-10-125-692-10
Sequence 10, Application US/10125692
Publication No. US2003004429A1
GENERAL INFORMATION:
APPLICANT: Aderem, Alan
APPLICANT: Hayashi, Fumitaka
APPLICANT: Smith, Kelly D.
APPLICANT: Underhill, David M.
APPLICANT: Ozinsky, Adrian
TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
FILE REFERENCE: P-15 5155
CURRENT APPLICATION NUMBER: US/10/125,692
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 60/285,477
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 612
TYPE: PRT
ORGANISM: Homo sapiens
US-10-125-692-10

Query Match 6.2%; Score 115; DB 9; Length 612;
Best Local Similarity 20.6%; Pred. No. 0.026;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

Oy 19 GAMGIVITGNHVSARIDDDHIVAPREPAITQLOLF---FMPGPRPKPYSGTVRAFR 75
Db 93 GSFPPLI---NKLKMDSSQYICLENKRE-EVILWYFKYTFSGTSLDQOSLTLTLDNS 149
Oy 76 SDITNOCYOELSEERFENCSTRSSSVFGCKVTETFSASRLTGPHHPKLTIRNPPN 135
Db 150 SKVSN---PLTE---CKHKKGVVSGSKV-----LSMSNLRYQ 181
Oy 136 DSGMFYIVRLDTPKEPIDVAIQLSYQFANTATRLYSKASCRTFGIPYQLEAYLR 195
Db 182 DSDFMNCTVTLQDK---NMFGMTLSVLGFQSTVAIT-AVKSDEESAEEFPLNFAF---- 233
Oy 196 TEESWRN--WOAVVATEATTSAEATTPPVATSSASELAEHTTPLENGVDHTEPT 253
Db 234 -ENGNGELMKKA-----EKDSFRPWSFSKKNVEVY 265
Oy 254 ANNSVTVRLGTMSPPLIGTVAAVVSATIGLVIVISYTRMCKTPHKKIDTVSODDEE 313
Db 266 QKSTKDLKQLKLTLPVLKIPQVSLQFAGSGL---TLTDKGLHDEVNLVYKVAQ 321
Oy 314 RSQTRRESKRFQPMVACEIN-----KGADD---SELVELVAIYNPSA----- 353
Db 322 LNNT-----LNCVEWGPSPKMRLLTQENQEARVSEQKYQVYVAPETGLMOCL 371
Oy 354 LSEPDGIRM 362
Db 372 LSEGDVKVM 380

PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,170
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 138
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (379)
OTHER INFORMATION: Xaa equals stop translation
US-09-813-153-138

Query Match
Best Local Similarity 23.6%; Pred. No. 0.2;
Matches 73; Conservative 36; Mismatches 133; Indels 67; Gaps 13;

QY 65 PYSGYVAVAFRSDITNOCYQELSEERFENCTHSSSVFVGCCKYTEYTFSSNRLTG--PP 122
DB 60 PYSGCKEALIRTD-----CMRVTSRK-SAKYRLQGTIPR 92

QY 123 HPRKLTIRNRPNDSGMFYIVRL---DDTKERIDVFAIQLSVOPANTATRGLYSKA 178
DB 93 GDVSLTILNPSDSGVCRIEYPCGFENDVK---INVLNL-QRASVTHRTATTTT 146

QY 179 SCRTFGILPTVQLEAVLRTESMRNMQAVVATEATTSAEATTPP-----VTATGASE 231
DB 147 RRTTTTSP-----TTROMTTTPALPTVVT--PDLTGTPLQMTIANTVTTTNTC 197

QY 232 LEAEHFTFPLENGVDHYETPTANENSNTVRLGTSPLIGTVAAVAGATGLVIVIS 291
DB 198 LSLTPSLP--EATGGLTPEPSKEGPILESEYVLPSSWSAESTSADTVLTSKES 255

QY 292 IYRNKCTPP---RKLDVTSODEERSOT---RRSRKFGPVACEIKGADDOSELY 343
DB 256 KAMDLPSTSHVSMKTSDSVSPQPGASDIAVEQKNTTGTGMDG--TMSKKNEMPIS 313

QY 344 ELVAIVNPS 352
DB 314 OLIMTIAPS 322

RESULT 7
US-09-801-366-332
Sequence 332, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patent In version 3.0
SEQ ID NO 332

LENGTH: 1220
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match
Best Local Similarity 22.7%; Pred. No. 3.3;
Matches 58; Conservative 43; Mismatches 104; Indels 50; Gaps 11;

QY 5 LGTLLAATLAFPGAGIYITGNHVSARIDDDHIVVAPRPEATIGLOLFMPGQPHK 64
DB 32 LGSLLIILAVT-----TGVFTSYVKNLR--SDRLYIAOLKSSQIDQTLNTL-----YQ 79

QY 65 PYSGYVAVAFRSDITNOCYQELSEERFENCTHSSSVFVGCCKYTEYTFSSNRLTG--PP 114
DB 80 AYLASRDALQSLTSYVACNKSADNVDSLVIQKFLSSNLFYVAKVYDSSFNAVLA 139

QY 115 SNRLTGPPH-----FKITIRNRPNDSGMFYIVRLDDTKERIDVFAIQLSVOPAN 167
DB 140 TNGGTGDLIPEDVLDLFLPLSTDTPLP--SSLETIGILTDPVINSTD-YLMSMSLPIFAN 196

QY 168 TAATRGLYSKASCRTEGLPTVQLEAVLRTESMRNMQAVVATEATTSAEATTPPTVAT 227
DB 197 PSII-----LTDSRVYGTITIIISA-----EGLKSVENDTTALEHSTIAITISAV 240

QY 228 SASELEAE--HFTFP 240
DB 241 YNSGKASGYHFVFP 255

RESULT 8
US-09-738-626-5621
Sequence 5621, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patent In Ver. 3.0
SEQ ID NO 5621
LENGTH: 320
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5621

Query Match
Best Local Similarity 20.6%; Pred. No. 1.2;
Matches 62; Conservative 46; Mismatches 109; Indels 84; Gaps 14;

QY 100 SYFVGCXYEY-----TFSSNRLTGPPH-----PRKLTIRNRPNDSGMFYIVRL 146
DB 56 AYFAPAEISHYMLVTFPA-----GLPHETIIPVAGPIPMHILTRDAEGNET-----KF 102

QY 147 DDTKEPIDVFAIQL---SVYOFANTATRGLYSKASCRTEGLPTVQLEA-YLRTESMRN 202
DB 147 DDTKEPIDVFAIQL---SVYOFANTATRGLYSKASCRTEGLPTVQLEA-YLRTESMRN 202

DB 103 KDSMPDLVSQLATLRDLVVRRAEDAAVLLGG-----NPSIAPAMFVDVVRSLRL 155
QY 203 KQAYVATEATTSTA-----EATPTPTAT-----ASELEAHEFTPEMLGVYDH 248
DB 156 VHPHVKAIAATGAALRAVIRLOLAATSPDALIVAAREIATATLEPKTLGCPWE----- 210
QY 249 VEPTPANENSVTVRLGTMSPTLIGTVAAVAVSATIGLVISITVRNMCPTPHKLDTPVS 308
DB 211 -----GDLSPV--AAARALIDSGVEVLTNKRTESLYVESESLIAS 252
QY 309 QDDERSQ--TRRESKFGVMACELNKGADDESEIVEIAIVNPSA-----LSSPDSI 360
DB 253 YSTPGKQGVNMRRESFTAGFLAAS--NDCKSTEDSVINAVAVANAGSMDVYIPTPKL 310
QY 361 K 361
DB 311 R 311

SUPT 9
Sequence 1, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borcun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448
TELEX: 25-3850
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 30..547
US-09-753-436-1

Query Match
Best Local Similarity 23.3%; Pred. No. 2.8;
Matches 69; Conservative 36; Mismatches 80; Indels 111; Gaps 15;

QY 103 VCGKTYEYTFSSNRLTGPPEPKL-----TIR-----NRPDSCMFYI 143
DB 98 VVNCNGSQITGSSNITVYGLPERVELAPLPMPQVGOFTLRQVEGGSPR--TSLIVYL 154
QY 144 VRLLD-----TREPIDVEAIDLS-----VGFANTATRGLY 175
DB 155 LRMEELRQPAVEPEPAVEATATVLAARDHGAPEFCRTEDMOPQIGLVNTSAPROL- 213
QY 176 SKASCRTEGTPV--OLEA--YLRTESW-----RMQAVYA--TEATT 214
DB 214 -----RTFLVPTPRLVAPRFLVETSWPVDCTLDGLFPASEAQVYALGDOMLNATVM 268
QY 215 SATATPTPTVATSALEA-----EHTF--FPMLENGVHYEPTPAN 255
DB 269 NHDDTLTATATATAAAGEGAREIVCNVTLGGERREARENITVVSFLGPTVNLSEPT-AH 327
QY 256 ENSNVTVRLGTMSPTLIGTVAAVAVSATIGLVISITVRNMCPTPHKLDTPVSODD 311
DB 328 EGSTVTV--SCMAGARQVITLDGVPAAAPGQ-----TAQLNLATRESDD 369

RESULT 10
US-09-870-759-73
Sequence 73, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 73
LENGTH: 365
TYPE: PRT
ORGANISM: Mus musculus
US-09-870-759-73

Query Match
Best Local Similarity 4.9%; Score 91; DB 9; Length 365;
Matches 78; Conservative 52; Mismatches 128; Indels 124; Gaps 19;

QY 50 TQDLFTMPQQRPHK-----YSGTVRV-----ARSDITNOGY 83
DB 15 LQSL-----AHPHQIDILANTCYRAGVHEKNGRYSISRTREADLCOARNSTLPTMDQ 69
QY 84 QELS-EERFENC-----THRSSVVGKAYE--YFFSASNN 117
DB 70 KMLASKGFTCYRGTGEGNVVTPRIHNAICANHTGYILVTSNTSHYDTYCFNNS-- 127
QY 118 LTGPPEPKLTLRN--PRPDSCMFYIVRLDTR-----EPIDVAIDLSYQF 165
DB 128 --APPEEDCVSYDLPNSFDGVPVTTIVNRDGTYSKKEGYRHOBDIDASNIT-----I 179

QY 166 ANTAATRGTSKASCRTFGLPTVOLAEYLTREESMRNM-----QAVVATEATTSAEAT 219
Db 180 DDVVSSSTETKSTPEYILHT-----YLPTEQPTGDQDSFIRSLATRDSDSSDR 234
QY 220 TTPPVATSASEDAEHFTFPMLENGVDHYEPANENSATVRLGTMSFTLG---VTV 276
Db 235 GSSR-TVTHGSEL-AGH-----SSANDSCVTTTSCPMRRPQIPEWILITL 277
QY 277 AAVVATIGVIVISTYTRMCTPHRKLDVTSQDDERSTRESRKFQMVACEINKA 336
Db 278 ASLALALILAVCIANSRRCOKKLL--VINGNGTVEDRKP-----ELNGEA 326
QY 337 DQSELVELVAIVNPALSPP 358
Db 327 SKQSEMYHL---VNKPERSETPD 345

RESULT 11
US-09-978-295A-45
Sequence 45, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivarov, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704

[illegible]

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.98; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.08; Pred. NO.2.4; 113; Indels 117; Gaps 16;
Matches 72; Conservative 41; Mismatches

5 LGTL---ALIAATLAPGAMGIVITGNHVSARIDDHIVAVPREATIOLOLF-----55
16 LGVLMVAMQMLLASFTLOCEBPVCT-ESSCHTEDD---LTDAREGFOVKATITSEP 70
56 -----FMFGORPHKP-YSGTVVAFRSDITNQCXYOLSEERFENCTHRSSVYVQCK 106
71 FHLIVYDWMLLQGPAPKPVFEGDLV---LRQAMQD-----WP 106
107 VTEYTFASNRITGPPHP---FKLTIIRNRPNDGMY-----VIVR 145
107 LQGVTFYRDSGALGPPGPNNRFSITV---VQKADSGHYHCSGIFQSPGPIPTASVAIT 164
146 LDD-----TREPIDVFAIOL---SVYQFANTATGELYSK 177
165 VOELFPAPILRAVPSAPQASPMILSCOTKILPQRSAALILSPFKDRIVOSGLSE 224
178 ASCRFGGLPTVQ-----LEAYLRTESNR-NMQAYVATEATTSAETTPTEVATS 228
225 -----FOIPFASDHSSGYCEAFATEDNOMVQSPQLEIRQASASSA-----APPTLPN 274
229 ASELEHETFPMLENGVDHYEPTPANENSNTVVLGTMSPTL 271
275 APOKSAAPCTAPEARPLPPTPSSEDPGSSPLGMPDPL 317

RESULT 13
US-09-978-192A-45
Sequence 45, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvarioff, Ellen
APPLICANT: Fong, Wei-Oliang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Selected and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Selected and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P103
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match

4.9% Score 90.5; DB 9; Length 359;

Best Local Similarity 21.0%; Pred. No. 2.4; Indels 117; Gaps 16;

Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

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DB 16 LGLVWQAQMLLASFETLQCEGPVCT-ESSCHTEDD-----LTDAREAGHYKAYFESPE 70
QY 56 -----FMPCGPRPKP-YSGTVRYAFRSDITNOCYQELSEBERFNCJHKSSVYGVCK 106
DB 71 FHLIVSYDWLILQGPAPKPFEGDLV-----LRCQAMOD-----NP 106
QY 107 VREYFESASNRLLGPPHP---FKLTIRNRPNDGMEY-----VIVR 145
DB 107 LTQVITYRQGSALGPPGNRESITV--VQKADSGHYHSGIFQSGPCGIPETASVAIT 164
QY 146 LDD-----TKEPIDVFATOL--SVYQFANTATRLGYSK 177
DB 165 VQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQKSAARLLSEFYKDGDRIVQSRLSSE 224
QY 178 ASCRTFGLPVVO-----LEAYLFTRESWR-NMQAYVATEATTTSACERTPTPTATIS 228
DB 225 -----FOIPTASEDHSGSYWCEATEDNQWKSPOLEIRVOGASSSA-----APPTLNP 274
QY 229 ASLEAEHFTFPWLENGVDHYEPTPANENSNNVVRGLTMSPTL 271
DB 275 APOKSAAPGTAPAEADPLPPPTPSSEDPGFSPLGMPDPHL 317

RESULT 14
US-09-999-832A-45
Sequence 45, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fond, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

Tue May 6 18:37:33 2003

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Page 11

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paooni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: us/09/999,832A
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1997-10-17
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Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred No. 2.4; Indels 117; Gaps 16;

Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

QY 5 LGTL---ALLAATLAFGAMGIVITGNHVSARIDDDHIVAPREATTIQLF-----55
DB 16 LGVLWVAOMLLASFETLOEGEPVCT--EESSCHTEDD---LTDAREAGFQVAVTPSEP 70
DB 56 -----FPGGQRPKHP-YSGTVRAVAFRSDITNOCYQELSEERFENCCTHRSSVPFGCK 106
DB 71 FHLIVSYDWLILLOGPAKPVFEGDLV-----LRCQAMQD-----WP 106
QY 107 VTEYTFASNRLLTGPPHP---FKLITRNPRPNDGMPY-----VIVR 145
DB 107 LTOVYTFYRDSGALGPEPNEFSITV--VOKADSGHYHCGITPQSGEPGIPETASVAIT 164
QY 146 LDD-----TRKPIDVFAIOL--SVYQFANTAAITRGLYSK 177
DB 165 VQELFAPRILRAVPSAPQAGSPMLTSCQKRLPLQSSAARLLPSFKDGHIVQSGISSE 224
QY 178 ASGRTGGLPVQ-----LEAVLRTESWR-NMQAYVATEATTTSAEATTPTPVATIS 228
DB 225 -----FOIPTASEDHSGSYWCEATEDNQWKOSPOLEIFVQASSSA-----APPTLNP 274
QY 229 ASLEAEHFFPWLGVNDHYEPTPANENSNVAVRLGTSPTL 271
DB 275 APOKSAAPGTAPEDAPRPLRPPTPSSEDDGFSPLGMPDPL 317

RESULT 15
US-09-978-189-45
; Sequence 45, Application US/09978189

;; Publication No. US20030004102A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
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;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2630PIC7
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PRIOR APPLICATION NUMBER:	60/0810707
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PRIOR APPLICATION NUMBER:	60/0819555
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/0818171
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PRIOR APPLICATION NUMBER:	60/0827991
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PRIOR APPLICATION NUMBER:	60/0834966
PRIOR FILING DATE:	1998-04-29
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PRIOR FILING DATE:	1998-04-29

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PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085700
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085689
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085579
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085580
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085573
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085704
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

Query Match
Best Local Similarity 4.9%; Score 90.5; DB 9; Length 359;
Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

OY 5 LGTL-----ALLAATLAPFGAMGIVITGNIVSARIDDDIYIVAPREAIOTLOF----- 55
Db 16 LGTLWAGMULLAASFETLQCEGVYV-ESSCHIEDD-----LIDAEAGFYKAVITSEP 70
OY 56 -----FMGCPHPK-YSGVYKAPAFSDITNOCQELSEBERFENCHSSYFVGCK 106
Db 71 FHLIYSDMLLQGAAPVEFEGULV-----LRCAMOD-----WP 106
OY 107 VLEYTPASNRLLTGPHP--FKLITRNDPNSGMFY-----YIVR 145
Db 107 LKQVTFYFDGSGALPQGNREFSITV--VOKADSGYHCSGIFQSPGCEIPETASVAIT 164
OY 146 LDD-----TRKPIEVAIQL--SVYOFANATIRGLYK 177
Db 165 VQELFPAPILRAVSAEPQASPMTLSCQTKLPQDRSAAARLLSFYKDRIRYOSGJSE 224

```

OY 178 ASCRTEGLPTVO-----LEAYLRTEESWR-NMOAYVATEATTSAEATTPPYTATS 228
Db 225 -----FOIPTASEDHSGSYWC EAATEDNOYWKOSPQLEIRVOGASSSA-----APPTLNP 274
OY 229 ASELEAHEFTFPWLENGVDHIEPTPANENSNTVRLGTMSPTL 271
Db 275 APQKSAAPGTAPPEAPGPLPPPTPSSEDDGFGSSPLGMPDPHL 317

Search completed: May 5, 2003, 16:26:32
Job time : 18.5 secs

Tue May 6 18:37:31 2003

us-09-993-777-68. rag

Page 1

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:02:52; Search time 53.5 Seconds
(without alignments)
901.621 Million cell updates/sec

Title: US-09-993-777-68

Perfect score: 1863

Sequence: 1 MASLCTALLAATLAPGA.....VELVAIVNPSALSPDSIKM 362

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

A.Geneseq.101002.*
1: /SID52/gcgdata/geneseq-emb1/AA1980.DAT.*
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23: /SID52/gcgdata/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	16	AAW0635 ILTV glycoprotein
2	1863	100.0	362	17	AAW06787 ILTV glycoprotein
3	156	8.4	384	15	AAW47236 Wild-type Feline H
4	152	8.2	355	18	AAW13105 Marek's disease vi
5	148	7.9	364	18	AAW11475 Canine herpesvirus
6	148	7.9	364	19	AAW22999 Canine herpes viru
7	148	7.9	364	22	AAW51316 Canine herpes virus
8	148	7.9	350	8	AAW0645 Pseudorabies virus
9	143.5	7.7	350	15	AAW63143 Glycoprotein 63 (g
10	143.5	7.7			

11	143.5	7.7	350	22	AAW05396	Pseudorabies virus
12	143	7.6	317	22	AAW0637	Bovine herpes viru
13	142.5	7.6	350	22	AAW04970	Pseudorabies virus
14	141.5	7.6	350	22	AAW82502	Pseudorabies virus
15	140.5	7.5	380	15	AAW8093	Sequence of polype
16	139	7.5	371	22	AAW8825	Pseudorabies virus
17	138	7.4	370	21	AAW32474	DNA encoding of tur
18	125	6.7	356	17	AAW03136	Herpesvirus of tur
19	125	6.7	356	17	AAW22323	Herpesvirus of tur
20	123.5	6.6	253	13	AAW33180	Mark Disease Virus
21	114	6.1	456	14	AAW33180	L3T4 mutant ML-5
22	112	6.0	387	20	AAW08621	Human secreted pro
23	112	6.0	387	21	AAW67312	Human secreted pro
24	109.5	5.9	454	14	AAW33181	L3T4 mutant M8 S
25	108.5	5.8	319	22	AAW69348	Drosophila melanog
26	108	5.8	713	16	AAW85878	MD-40 domain SRS C
27	107	5.7	372	19	AAW72164	HSV-2 strain SRS C
28	107	5.7	433	19	AAW72164	HSV-2 strain SRS C
29	107	5.7	433	19	AAW72012	Human polypeptide
30	105.5	5.7	378	22	AAW39027	Drosophila melanog
31	103	5.5	982	22	AAW58158	Human secreted pro
32	102.5	5.5	379	20	AAW25768	Human secreted pro
33	102.5	5.5	4498	22	AAW58595	Human ORF2880 prot
34	102	5.5	234	12	AAW4768	Metastasis-specifi
35	98	5.3	503	12	AAW60186	Human novel polype
36	97.5	5.2	1714	22	AAW60186	Drosophila melanog
37	96	5.2	1296	23	AAW66702	Human novel polype
38	96	5.2	1296	23	AAW66702	Human novel polype
39	95	5.1	745	22	AAW71016	Urosophila melanog
40	94.5	5.0	307	19	AAW38334	Rat kidney injury
41	94	5.0	886	22	AAW64308	Drosophila melanog
42	93.5	5.0	907	6	AAW50073	Epsstein-Barr virus
43	93.5	5.0	907	16	AAW80144	Epsstein-Barr virus
44	93.5	5.0	907	21	AAW68009	Epsstein-Barr virus
45	93	5.0	320	22	AAW31867	C glutathione prote

ALIGNMENTS

RESULT 1	
ID	AAW0635 standard: Protein: 362 AA.
AC	AAW0635;
DT	19-NOV-1996 (first entry)
XX	ILTV glycoprotein gi.
DE	Infectious laryngotracheitis virus; ILTV; herpesvirus;
XX	attenuation; vector; vaccine; chicken; poultry; immunisation;
KW	glycoprotein gi.
KW	Infectious laryngotracheitis virus.
OS	Infectious laryngotracheitis virus.
XX	
PN	WO9508622-A1.
ED	30-MAR-1995.
XX	
PF	16-SEP-1994; 94WO-US10628.
XX	
PR	24-SEP-1993; 93US-0126597.
XX	
PA	(SYTR) SYNPRO CORP.
XX	
PI	Cochran MD, Wild MA;
XX	
DR	WPI: 1995-139591/18.
DR	N-PsDB: AAT33504.
XX	
PT	Recombinant attenuated infectious laryngotracheitis virus - for use in vaccines to protect poultry from infection from the virus; also

Pseudorabies virus
Bovine herpes viru
Pseudorabies virus
Pseudorabies virus
Sequence of polype
Pseudorabies virus
DNA encoding of tur
Herpesvirus of tur
Mark Disease Virus
L3T4 mutant ML-5
Human secreted pro
Human secreted pro
L3T4 mutant M8 S
Drosophila melanog
MD-40 domain SRS C
HSV-2 strain SRS C
HSV-2 strain SRS C
Human polypeptide
Drosophila melanog
Human secreted pro
Human secreted pro
Human ORF2880 prot
Metastasis-specifi
Human novel polype
Drosophila melanog
Human novel polype
Urosophila melanog
Rat kidney injury
Drosophila melanog
Epsstein-Barr virus
Epsstein-Barr virus
Epsstein-Barr virus
C glutathione prote

PT methods of distinguishing between vaccinated and naturally infected
PT birds
XX
PS Example 1; Page 102-103; 177pp; English.
XX
CC The gi gene, spanning nucleotides 9874-10962 of the unique short
CC region (AAT33504) of infectious laryngotracheitis virus (ILT),
CC codes for a glycoprotein (AAM0635) of approx. 39,755 mol.wt.
CC The gi glycoprotein is homologous to Varicella-zoster gi.
CC Deletion of the gi gene results in an attenuated ILTV that
CC is useful as a vaccine against ILT disease in chickens.
CC Recombinant virus deleted for gi was safe in animal trials.
CC Deletion of the gi gene serves as a negative marker to
CC distinguish vaccines from infected animals. A gene coding
CC for a foreign antigen may be inserted into the gi gene to
CC produce a recombinant multivalent vaccine.
XX
SQ Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 16; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATIQLDFMPGQ 60
DB 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATIQLDFMPGQ 60
OY 61 RPKRPVSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCAYTEYTFASNRITG 120
DB 61 RPKRPVSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCAYTEYTFASNRITG 120
OY 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
DB 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
OY 181 RTFGLPTVLEAVLRTREESRMNOAVVATEATTSAETPPVTATSSASEAHEHTFP 240
DB 181 RTFGLPTVLEAVLRTREESRMNOAVVATEATTSAETPPVTATSSASEAHEHTFP 240
OY 241 WLENGVDHYEPPPANENSNTVRLGTMSPLIGVTAAVASATIGIYIYSITRNKCP 300
DB 241 WLENGVDHYEPPPANENSNTVRLGTMSPLIGVTAAVASATIGIYIYSITRNKCP 300
OY 301 HRKLDIVSODDEERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDEERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
OY 361 KM 362
DB 361 KM 362

RESULT 2
AAM06787
ID AAM06787 standard; Protein: 362 AA.
XX
AC AAM06787;
XX
DT 02-JUN-1997 (first entry)
XX
DE ILTV glycoprotein gi.
XX
KM ILTV; vaccine; vector; attenuation; poultry;
KM avian infectious bronchitis virus; Newcastle disease virus;
KM infectious bursal disease virus of chickens;
KM Marek's disease virus; herpesvirus; glycoprotein gi.
XX
OS Infectious laryngotracheitis virus USDA strain 8302.
XX
FH Key Location/Qualifiers
FT Peptide 1..22
FT Protein /label= sig-peptide
FT 23..362

PT
FT Region /label= Mat_protein
FT 272..292
XX /label= Transmembrane_helix
XX
PN MO9629396-A1.
XX
PD 26-SEP-1996.
XX
PF 21-MAR-1996; 96WO-US03916.
XX
PR 06-JUN-1995; 95US-0468190.
PR 23-MAR-1995; 95US-0410121.
XX
PA (SYTR) SYNTRO CORP.
PI Cochran MD, Wild MA;
XX
DR WPI; 1996-443172/44.
DR N-PSDB; AAT44384;
DR N-PSDB; AAT44385.
XX
PT Recombinant infectious laryngotracheitis virus with deletion in the
PT glycoprotein G₁ or us2 gene, etc. - useful for vaccines against
PT infectious laryngotracheitis in poultry
XX
PS Example 11; Page 110-111; 216pp; English.
XX
CC Glycoprotein gi (AAM06787) is encoded by ORF8 of the unique short
CC region (AAT44384) of infectious laryngotracheitis virus (ILT). It
CC shows homology to the Varicella zoster virus gi glycoprotein.
CC Recombinant ILTV gi protein produced in a swinepox virus reacts to
CC convalescent sera from ILTV-infected chickens. Deletion of the gi
CC gene results in an attenuated ILTV that is useful as a vaccine and
CC as a negative marker to distinguish vaccines from infected
CC animals. Insertion of a foreign gene into the gi gene allows
CC prodn. of multivalent vaccines.
XX
SQ Sequence 362 AA:

Query Match 100.0%; Score 1863; DB 17; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.7e-174;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATIQLDFMPGQ 60
DB 1 MASLGTLLAATLAPFGAMGIVITGNHVSARIDDDHIYVAPREATIQLDFMPGQ 60
OY 61 RPKRPVSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCAYTEYTFASNRITG 120
DB 61 RPKRPVSGTVRAVFRSDITNOCYQELSEERFENCSTRSSVFVGCAYTEYTFASNRITG 120
OY 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
DB 121 PPHPKFLITRNPRPNDSCGFYIVRLDDTKEPIDVFAIQLSVQFANTATRLYSKASC 180
OY 181 RTFGLPTVLEAVLRTREESRMNOAVVATEATTSAETPPVTATSSASEAHEHTFP 240
DB 181 RTFGLPTVLEAVLRTREESRMNOAVVATEATTSAETPPVTATSSASEAHEHTFP 240
OY 241 WLENGVDHYEPPPANENSNTVRLGTMSPLIGVTAAVASATIGIYIYSITRNKCP 300
DB 241 WLENGVDHYEPPPANENSNTVRLGTMSPLIGVTAAVASATIGIYIYSITRNKCP 300
OY 301 HRKLDIVSODDEERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDEERSQTRRSRKFQPMVACEINKGADDOSELVELVAIVNPSALSSPDSI 360
OY 361 KM 362
DB 361 KM 362

RESULT 3

AA047236
ID AA047236 standard; Protein; 384 AA.
XX
AC AA047236;
XX
DT 06-SEP-1994 (first entry)
XX
DE Wild-type Feline Herpes Virus ORF-1-encoded protein.
XX
KW Feline herpes virus; FHV; genome; mutant; vaccine; ORF-1;
XX
KW Feline viral rhinotracheitis; herpesviridae family;
XX
KW herpes virus A subfamily.
XX
OS Feline Herpes Virus.
XX
PM M09403621-A.
XX
PD 17-FEB-1994.
XX
PF 23-JUL-1993; 93MO-EP01971.
XX
PR 30-JUL-1992; 92BP-0202365.
XX
PA (ALKU) AKZO NV.
XX
PI Sondermeijer PJA, Willemsse MJ;
XX
DR WPI: 1994-065709/08.
XX
DR N-PSDB; AAO56188.
XX
PT Feline herpes virus mutant comprising a heterologous gene
PT inserted in the virus genome - for vaccination against feline
PT herpes virus and other feline pathogens.
XX
PS Claim 2; Page 37-38; 55pp; English.
XX
CC Mutant versions of the wild-type feline herpes virus genome (AA056188)
CC are claimed. Esp. the FHV mutant is one which fails to produce one
CC or more antigenic or functional polypeptides. The mutant may contain
CC a heterologous nucleic acid sequence inserted within one of the 6
CC open reading frames. The attenuated FHV mutants can be used to prepare
CC vaccines against feline viral rhinotracheitis and, where the
CC heterologous insert encodes an antigen of a feline pathogen,
CC against other infectious diseases of feline.
XX
SQ Sequence 384 AA;
Query Match 8.4%; Score 156; DB 15; Length 384;
Best Local Similarity 23.3%; Pred. No. 1.6e-06;
Matches 75; Conservative 48; Mismatches 141; Indels 58; Gaps 12;
OY 5 LGTLLAATLAPRGAMGIVITGNHVSARIDDDHIVAPRPE-ATIQLOLFPMGQ-RP 62
DB 1 MSIAFIYIIMAGTGYCYIRGDHVSIAVDTSQFVYPTLENTIYGLIFLDQPLP 60
OY 63 HKPYSGTVAVAFRSDITNOCYQELSEFRENCTHRSSVFGC--KYTEYFSASNRITG 120
DB 61 VNNYNGTLET-IHNNHSCYKIYOYIESSCPVRNNAPRSCILHSMHOYDLSINTS 119
OY 121 PPHPELITRNPRFDSGMFYIVRIDTKERIDVEALQSYQFANTATRGYSKASC 180
DB 120 VETGMLLTTSFKMEDGITALRFRNNHKK-ADYFGISYVYSF-----DTGHHND- 173
OY 181 RTGGLPTVQLEAYLTETESRNQAVATFATTTSAEATPTTPTVATSSSEAEHFTFP 240
DB 174 -----ENLNGEILTPS--SMETVYKVNPIYDHMYTDT-----TSKSMSE--P 216
OY 241 MLENGVHYEPTPANENSNTVRL-----GTMSPLIGYVAANYAT- 283
DB 217 SNTISCHTFONDPRNEGTELTTHLLNAGNITYDDVMGDTTLPRLIDGLNLSYSF 276
OY 284 -----IGLVIVISI 292

DB 277 KNETTOKWTFPDRKVGFIIVISI 298
RESULT 4
ID AA013105
XX
AC AA013105 standard; Protein; 355 AA.
XX
DT 12-MAY-1997 (first entry)
XX
DE Marek's disease virus type 1 glycoprotein I.
XX
KW Marek's disease virus; gpi; gpE; recombinant virus;
XX
KW GA strain; glycoprotein; gpi; gpE; recombinant virus;
XX
KW Newcastle disease virus; herpes virus; vaccine.
XX
OS Marek's disease virus type 1.
XX
PM JF09009978-A.
XX
PN 14-JAN-1997.
XX
PD 26-APR-1996; 96JP-0131084.
XX
PF 28-APR-1995; 95JP-0129523.
XX
PR (JAPG) JAPANESE GEON CO LTD.
XX
PA WPI: 1997-126432/12.
XX
DR N-PSDB; AAT61883.
XX
PT Recombinant virus contg. herpes virus glyco:protein gE - and
PT effective Newcastle disease vaccine contg. It
XX
PS Claim 5; Pages 14-15; 20pp; Japanese.
XX
CC The present sequence encodes the Marek's disease virus (MDV) type 1
CC (GA strain) glycoprotein (gpi) I. A recombinant virus containing the
CC gene encoding MDV gpE, and optionally also gpi, in a genomic region
CC unessential for its growth, can be used as the effective component
CC in a Newcastle disease virus vaccine.
XX
SQ Sequence 355 AA;
Query Match 8.2%; Score 152; DB 18; Length 355;
Best Local Similarity 22.9%; Pred. No. 3.5e-06;
Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;
OY 19 GAMGIVITGNHVSARIDDDHIVAPRPE-ATIQLOLFPMGQRPKPYSGTVAVAFRSD 77
DB 15 GIMSVITGTSVLTSDQSAIYAFGCDPKMNVNRGOLFLGDTRTSYTGTETI-LKWD 73
OY 78 ITNOCYQELSEFRENCTHRSSVFGCKYETFSASNRILGPRPHPK--LTIRNRP 134
DB 74 EYKCYSTVLAHSTYMCPRADIDATVPRGCRDAVYVYAOHRDV--OPPEKGTLLRIYEPV 131
OY 135 NDGMEFYIVRLDDTKERIDVEALQSYQFANTATRGYSKASCRTFGPLTVQLEAYL 194
DB 132 SPTGSYTVRAVLAG-RMSDIFRMVILRS-----SKSNACNHSAS9FQAHKCI 179
OY 195 RTEE--SWRNQAVATFATTTSAEATPTTPTVATSSSEAEHFTFPMLNGVDHYEPT 252
DB 180 RYVDMAEENLIGHGNLDSSELAHIVITQSS-ITDNIITTFYNSCTIYSP 238
OY 253 P---ANENSNTVRLGT-MSPLIGYVAANY--SATIGLVY---ISIVRNKCTPHK 303
DB 239 VFNLNNSHVDANSTGMNNTVLKTYLPRILYSTNIVICLIALAIVYVCEKRGSRHR 298
OY 304 LDTVSODDEERSQTRRESKFGPMVACEINKGADOSELYE 344
DB 299 I-----YIGPRSD-----APLITSAVNESFOYDYNKE 328

[illegible]

Db	299	I----	YIGEPNRSD-----	APLITSVNESFQDYNNKE	328
		RESULT 6			
		AAW22999			
ID		AAW22999	standard; Protein: 364 AA.		
XX		AC			
XX		AAW22999;			
XX		20-FEB-1998	(first entry)		
XX		DE	Canine herpesvirus glycoprotein I PCg1364.		
XX		KW	Vaccine; vector; gene therapy; canid; dog; CHV; Cg1; PCg1364;		
XX		KW	glycoprotein I.		
XX		OS	Canine herpesvirus.		
XX		PN	WO9729772-A1.		
XX		PD	21-AUG-1997.		
XX		PF	14-FEB-1997; 97WO-US04115.		
XX		PR	15-FEB-1996; 96US-0602010.		
XX		PA	(HESK-) HESKA CORP.		
XX		PI	Frank RA, Heanes EJ;		
XX		DR	WPI; 1997-424756/39.		
XX		DR	N-PSDB: AAT75616.		
XX		PT	Recombinant canine herpes virus and its genome - useful as vaccine		
XX		PT	to protect canids against infectious, metabolic or genetic diseases		
XX		PS	Claim 57; Page 181-182; 240pp; English.		
XX		BS			
XX		CC	This protein comprises canine herpesvirus (CHV) glycoprotein I		
XX		CC	(PCg1364). Its sequence was deduced from a coding region found in		
XX		CC	CHV genomic DNA molecule ncUS10592 (see AAT75616). PCg1364 can be		
XX		CC	expressed in transformed host cells. CHV proteins, nucleic acids,		
XX		CC	and antibodies raised against CHV proteins, can be used to protect		
XX		CC	canids against CHV infection. Novel recombinant CHV and novel		
XX		CC	recombinant CHV genomes that contain heterologous nucleic acid		
XX		CC	molecules inserted e.g. into Cgi gene, can be used as vaccines to		
XX		CC	protect canids against infectious, metabolic or genetic diseases.		
XX		SO			
		Sequence	364 AA;		
		Query Match	7.9%; Score 148; DB 18; Length 364;		
		Best Local Similarity	27.3%; Pred. No. 8.9e-06;		
		Matches	45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;		
Yy		4	LLGTALLAATLAPAGAGIVTGNHVSARIDDDHIVVADPREATTIOLQLFFMPGQR-P 62		
Db		16	LLITMFLRILFLFLXGVNGFYKGYIIMFLNTSGSGLFFDDKRTVSGRLFLDDQHLS 75		
Oy		63	HKPYSGIVAVAFRSDITNOCYQELSEERFENCNHRSSSVFVGC--KTEYTFASNRLTG 120		
Db		76	VNNNSCTVYQTIIEF--HFNNSCTVYQTIIEFYFSCPRIFNNAFSCLEKYSKHNHESQIRINS 132		
Oy		121	PRHPRKLTIRNPRNDSCGFVYIVLDDTKEDIDFAQLDSYQF 165		
Db		133	IENGVLEITNPKFMDSGVIFIRVQLENNK--TDVFGIPAFIYSF 175		
RESULT 7					
AAW22659					
ID		AAW22659	standard; Protein: 364 AA.		
XX		AC			
XX		AAW22659;			
XX		AC			

DT 07-JAN-1999 (first entry)
 XX Canine herpes virus protein sequence PC91-364.
 DE
 XX Canine herpes virus; CHV; recombinant canine herpes virus vector;
 KW genome; vaccination; dog; protozoan; helminth; ectoparasite; bacteria;
 KM virus infection.
 XX
 OS Canine herpes virus.
 XX
 PN US5804197-A.
 XX
 PD 08-SEP-1998.
 XX
 PF 12-JUL-1996; 96US-0680726.
 XX
 PR 12-JUL-1996; 96US-0680726.
 PR 13-FEB-1996; 96US-0602010.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Frank RS, Haanes EJ;
 XX WPI: 1998-505590/43.
 DR N-PSDB; AAV66941.
 XX
 PT Canine herpes virus nucleic acids - useful for producing recombinant
 PT canine herpes virus vectors
 PS Claim 7; Column 133-136; 103pp; English.
 CC The present sequence represents a canine herpes virus (CHV) protein
 CC acid. The nucleic acid sequence which encodes the protein can be
 CC used for DNA vaccination of dogs against CHV and also other infective
 CC agents such as protozoans, helminths, ectoparasites, bacteria and
 CC viruses. CHV can be formulated by incorporation of heterologous nucleic
 CC acid molecules as a single multivalent therapeutic composition against
 CC a variety of canine pathogens.
 XX
 SO Sequence 364 AA;
 Query Match 7.9%; Score 148; DB 19; Length 364;
 Best Local Similarity 27.3%; Pred. No. 8.9e-06;
 Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
 OY 4 LGCTLALATLAPGAMGIVITGNHVSARIDDDHIVVAPREATIQLOLFPMGQR-P 62
 16 LITIMFLPILFLFVGVNGFYVKGTYISWELMTSSGFSIFPDCKFVSGRLFLDDQHL 75
 OY 63 HKPYSGTVAVAFRSDITNOCYOLSEEFENCTHSSSVFVC--KTEYTFASNRLTG 120
 DB 76 VNNYSCTIEFI--HFNNSCTVYQTEIEFSCPRIFNNAFRCLKVKSHHESQLRINS 132
 OY 121 PPHPFKLTIRNRPNDSCMFYVIVRLDDTKREPIDVFAIOLSVYOF 165
 DB 133 IENGVLLEITNRPNDSCGFYFVROLENK--TDVFGIPAFIYTSF 175
 RESULT 8
 AAB51316
 ID AAB51316 standard; Protein: 364 AA.
 XX
 AC AAB51316;
 XX
 DT 29-MAR-2001 (first entry)
 XX
 DE Canine herpes virus protein sequence SEQ ID NO:56.
 KW Canine herpes virus; CHV; antiallergic; immunosuppressive; cytostatic;
 KM antibacterial; antiinflammatory; vaccine; candid; infectious disease;
 KW genetic disease; metabolic disease; abnormal cell growth; allergy;
 KM degenerative process; immunological defect; autoimmune disease; cancer;
 KM cardiovascular disease; graft rejection; hematopoietic disorder;

KW immunodeficiency disease; immunoproliferative disease; septic shock;
 KM immunosuppressive disorder; inflammatory disease; jaundice.
 XX
 OS Canine herpes virus.
 XX
 PN US6159478-A.
 XX
 PD 12-DEC-2000.
 XX
 PF 29-JAN-1998; 98US-0092409.
 XX
 PR 12-JUL-1996; 96US-0680726.
 PR 15-FEB-1996; 96US-0602010.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Frank RS, Haanes EJ;
 XX WPI: 2001-090270/10.
 DR N-PSDB; AAF26761.
 XX
 PT Novel recombinant canine herpes virus protein useful for protecting
 PT animals, in particular candid from herpes virus infection and various
 PT diseases including cancer and autoimmune diseases
 XX
 PS Example 10; Column 135-136; 101pp; English.
 CC The present invention describes an isolated canine herpes virus (CHV)
 CC (1) CDUPase protein encoded by a CHV nucleic acid molecule that
 CC hybridises under stringent hybridisation conditions with the CDUPase
 CC gene. Also described is a therapeutic composition (ii) comprising (i),
 CC (1) has antiallergic, immunosuppressive, cytostatic, antibacterial and
 CC antiinflammatory activities, and can be used in vaccines. (i) is useful
 CC for protecting an animal, in particular a candid from CHV. Therapeutic
 CC compositions comprising (i) are used in diseases including infectious
 CC genetic diseases and other degenerative processes and/or
 CC immunological defects including allergies, autoimmune diseases,
 CC cancers, cardiovascular diseases, graft rejection, hematopoietic
 CC disorders, immunodeficiency diseases, immunoproliferative diseases,
 CC immunosuppressive disorders, inflammatory diseases, jaundice, and septic
 CC shock. CHV need not be attenuated for use as a live vaccine vector due
 CC to the low pathogenicity of natural CHV particularly as compared to
 CC AAB51327 represent CHV nucleotides, proteins and PCR primers used in the
 CC exemplification of the present invention.
 XX
 SO Sequence 364 AA;
 Query Match 7.9%; Score 148; DB 22; Length 364;
 Best Local Similarity 27.3%; Pred. No. 8.9e-06;
 Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;
 OY 4 LGCTLALATLAPGAMGIVITGNHVSARIDDDHIVVAPREATIQLOLFPMGQR-P 62
 16 LITIMFLPILFLFVGVNGFYVKGTYISWELMTSSGFSIFPDCKFVSGRLFLDDQHL 75
 OY 63 HKPYSGTVAVAFRSDITNOCYOLSEEFENCTHSSSVFVC--KTEYTFASNRLTG 120
 DB 76 VNNYSCTIEFI--HFNNSCTVYQTEIEFSCPRIFNNAFRCLKVKSHHESQLRINS 132
 OY 121 PPHPFKLTIRNRPNDSCMFYVIVRLDDTKREPIDVFAIOLSVYOF 165
 DB 133 IENGVLLEITNRPNDSCGFYFVROLENK--TDVFGIPAFIYTSF 175
 RESULT 9
 AAP70645
 ID AAP70645 standard; Protein: 350 AA.
 XX
 AC AAP70645;
 XX
 DT 29-APR-1991 (first entry)

```

XX DE Pseudorabies virus gp63 protein.
XX XX PRV; vaccine; GI: gp50; gp63.
XX OS Pseudorabies virus.
XX PN W08702058-A.
XX XX
XX PD 09-APR-1987.
XX XX
XX PF 28-AUG-1986; 86WO-US01761.
XX XX
XX PR 16-JUL-1986; 86US-0886260.
XX PR 04-OCT-1985; 85US-0784787.
XX PR 26-NOV-1985; 85US-0801799.
XX PR 26-MAR-1986; 86US-0844113.
XX PR 26-MAR-1986; 86US-0844133.
XX XX
XX PA (UPJO ) UPJOHN CO.
XX PA (PETR/) PETROVSKIS E A.
XX XX
XX DR Petrovskis EA, Post LE, Timmins JG;
XX DR WPI: 1987-108699/15.
XX DR N-PSDB; AAN70994.
XX XX
XX PT Pseudo-rabies virus protein - produced from recombinant DNA and
XX PT used to produce vaccine and detect animals infected with virulent
XX PT virus.
XX PS Claim 8; Page 59; 67pp; English.
XX XX
XX CC The PRV glycoprotein product may be used as in vaccination of
XX CC animals such as swine, sheep and goats against infection by the
XX CC virus. The protein may be produced from a transformed expression
XX CC system such as E.coli, yeast or CHO cells operatively linked to a
XX CC suitable expression control sequence. Glycoproteins gp1 and gp63 may
XX CC be used to distinguish between infected and vaccinated animals.
XX CC See also AAN70993-5.
XX CC
XX SQ Sequence 350 AA;
XX
XX Query Match 7.7%; Score 143.5; DB 8; Length 350;
XX Best Local Similarity 22.8%; Pred. No. 2.3e-05;
XX Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
XX
XX QY 8 LALLAATLAFPGAM--GIVITGNHVSARIDDDHIVVAPRPEATIQQLFPMGQREHPR 65
XX Db 15 LLLAALTLAALTPRVGVLFRGAGSVHAGSAVLVPGDAPNLTIDGTLFLFEGSPSPN- 73
XX QY 66 YSGTVRAFRSDITNOCYQELSEERFENCNHRSSSVFVC--KVTEYTFGAS-----NRL 118
XX Db 74 YSGRVEL-LRLDPRKACTYREYAEYDLCPRVHHEAFRGCLRREPLARRASAAVEARRL 132
XX QY 119 TGPFRPFKLTIRNPRDSCMFYIVRLDPTKEPIDVFAQLSVYQFANRATRGRL---- 174
XX Db 133 -----LFSVRPAPPDAGSYLVLRVNGT---TDLEFVLTALV-----PRGRPHR 174
XX QY 175 --YSKASCRFTFGLPTVQLEAYLRTESWRMNAV--ATEATTSA-----EATPTPV 224
XX Db 175 TPSSADECR---PVV-----GSMHSLRVDPADAEAVTTTPPIPEPTTPAP 221
XX QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPFLIGVYA 277
XX Db 222 RGTGATPEPRSDDEDEDE-----EGATJAMTPVPETLDANGTM---VLNASVSVLL 271
XX QY 278 AVVSATIG-----LVYISIVTRNMCTPHRKLDTVVSODDERSCOTRRESRK 323
XX Db 272 AANAATAGARGPKIAMVGLPTIVLLIFLGVAACARCARCARGIASTGRDPCGAARSTR 331
XX RESULT 10

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AAR63143
XX ID AAR63143 standard; Protein: 350 AA.
XX XX
XX AC AAR63143;
XX XX
XX DT 12-JUN-1995 (first entry)
XX XX
XX DE Glycoprotein 63 (gp63) of pseudorabies virus.
XX XX
XX KM Pseudorabies virus; PRV; glycoprotein; gp50; GI: gp63;
XX KM determination; detection; vaccine; infected animal; isolation;
XX KM cloning; virulence.
XX XX
XX OS Pseudorabies virus.
XX OS
XX PN US5352575-A.
XX XX
XX PD 04-OCT-1994.
XX XX
XX PF 04-OCT-1985; 85US-0784787.
XX XX
XX PR 04-OCT-1985; 85US-0784787.
XX PR 26-NOV-1985; 85US-0801799.
XX PR 26-MAR-1986; 86US-0844113.
XX PR 16-JUL-1986; 86US-0886260.
XX PR 29-JUN-1987; 87US-0100817.
XX PR 20-APR-1990; 90US-0513282.
XX XX
XX PA (UPJO ) UPJOHN CO.
XX XX
XX PT Petrovskis EA, Post LE, Timmins JG;
XX PT
XX DR WPI: 1994-316176/39.
XX DR N-PSDB; AAO73489.
XX XX
XX PT Identifying animals vaccinated against pseudorabies virus - by
XX PT detecting the absence of GI or GP.63 antibodies in serum to
XX PT distinguish vaccinated from infected animals
XX XX
XX PS Example 3; Column 21-24; 21pp; English.
XX XX
XX CC AAR63143 shows the protein sequence of gp63 (glycoprotein) encoded by
XX CC AAO73489, isolated from Pseudorabies virus (PRV). The DNA and protein
XX CC sequences of the invention are useful in a method for distinguishing an
XX CC animal vaccinated with a PRV vaccine lacking glycoprotein GI, GP63 or
XX CC GP50 from an animal infected with a virulent wild-type PRV without
XX CC sacrificing the animal. The method is used to test animals such as
XX CC swine, cattle, sheep and goats. (see AAR63142 and AAR63144).
XX CC
XX SQ Sequence 350 AA;
XX
XX Query Match 7.7%; Score 143.5; DB 15; Length 350;
XX Best Local Similarity 22.8%; Pred. No. 2.3e-05;
XX Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
XX
XX QY 8 LALLAATLAFPGAM--GIVITGNHVSARIDDDHIVVAPRPEATIQQLFPMGQREHPR 65
XX Db 15 LLLAALTLAALTPRVGVLFRGAGSVHAGSAVLVPGDAPNLTIDGTLFLFEGSPSPN- 73
XX QY 66 YSGTVRAFRSDITNOCYQELSEERFENCNHRSSSVFVC--KVTEYTFGAS-----NRL 118
XX Db 74 YSGRVEL-LRLDPRKACTYREYAEYDLCPRVHHEAFRGCLRREPLARRASAAVEARRL 132
XX QY 119 TGPFRPFKLTIRNPRDSCMFYIVRLDPTKEPIDVFAQLSVYQFANRATRGRL---- 174
XX Db 133 -----LFSVRPAPPDAGSYLVLRVNGT---TDLEFVLTALV-----PRGRPHR 174
XX QY 175 --YSKASCRFTFGLPTVQLEAYLRTESWRMNAV--ATEATTSA-----EATPTPV 224
XX Db 175 TPSSADECR---PVV-----GSMHSLRVDPADAEAVTTTPPIPEPTTPAP 221
XX QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPFLIGVYA 277
XX Db 175 TPSSADECR---PVV-----GSMHSLRVDPADAEAVTTTPPIPEPTTPAP 221
XX QY 225 TATSAS-----ELEAHEFTFPMLENGVDHYEPTPANENSNTVRLGTMSPFLIGVYA 277

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DB 222 RGTGATPEPRSDDEEED-----EGATTANTPVPGTLDANGTM--VUNASVSVRLV 271
OY 278 AVSATIG-----LVIVISIVTRNMCTPHKLDTVSODDEBSQTRRESRK 323
DB 272 AAANATGARGPGKIAMVIGPTIVLLIFLGVAACARCAARGIASTGRDPAARRSTR 331

RESULT 11
AAE05396 standard; Protein: 350 AA.
ID AAE05396
XX
AC AAE05396;
XX
DE 24-SEP-2001 (first entry)
XX
DE Pseudorabies virus (PRV) glycoprotein gp63.
XX
DE Pseudorabies virus; PRV; glycoprotein; gp63; immunostimulant; vaccine;
XX PRV infection.
XX
XX Pseudorabies virus.
XX
XX Key Location/Qualifiers.
FH Misc-difference 131 /note- "Encoded by GCG"
FT Misc-difference 132 /note- "Encoded by GTG"
FT Misc-difference 144 /note- "Encoded by CCG"
FT Misc-difference 207 /note- "Encoded by CCG"
FT Misc-difference 222 /note- "Encoded by GCG"
FT Misc-difference 223 /note- "Encoded by GCG"
FT Misc-difference 284 /note- "Encoded by CCG"
FT Misc-difference 334 /note- "Encoded by GCC"
FT Misc-difference 334 /note- "Encoded by GCC"
XX
XX US6261563-B1.
XX
XX 17-JUL-2001.
XX
XX 07-JUN-1995; 95US-0485287.
XX
XX 20-APR-1990; 90US-0513282.
XX 21-JUN-1994; 94US-0262813;
XX 28-AUG-1986; 86MO-0501761.
XX 28-NOV-1985; 85US-0801799.
XX 28-MAR-1986; 86US-0844113.
XX 16-JUL-1986; 86US-0886260.
XX 29-JUN-1987; 87US-0100817.
XX
XX (PHMA ) PHARMACIA & UPJOHN CO.
XX
XX Petrovskis EA, Post LE, Timmins JG;
XX
XX WPI: 2001-450478/48.
XX
XX N-PSDB: AAD10195.
XX
XX Polypeptide comprising a pure and isolated pseudorabies virus gp63
XX polypeptide or its fragments, useful as a vaccine for protecting
XX animals against pseudorabies virus infection.
XX
XX Claim 1: Column 39-40; 21pp; English.
XX
XX The invention relates to Pseudorabies virus (PRV) glycoproteins gp50,
XX gp63, gI and their corresponding DNA molecules. These glycoproteins are
XX used as vaccines for protecting animals against PRV infection.
XX The invention also relates to methods for protecting animals against PRV
XX infections and methods for distinguishing between infected and vaccinated
XX animals. The present sequence is Pseudorabies virus (PRV) glycoprotein

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CC 9p63.
XX
XX Sequence 350 AA:
SO
Query Match 7.7%; Score 143.5; DB 22; Length 350;
Best Local Similarity 22.8%; Pred. No. 2.3e-05;
Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

OY 8 LALLAATLAPFGAM--GIVITGNHVSARIDDIHIVAVRPPATITQLOLFMPGQRPHP 65
DB 15 LLLAALLTALPRVGVLFPRGACVSVHAGSVAVLPAGDAPMLTIDGTLLEBPSPSN- 73
OY 66 YSGTVAVRPSDITNOCYOELEERFENCNHRSSVFVC--KVLEYFEAS-----NRL 118
DB 74 YSGRVEL-LRLDPKACVTRREYAEYDLCPRVHNEAFRCCLRKREPLARASAAVEARRL 132
OY 119 TGPPHPFKLTIRPNPNSGMFYIVRLDPTKEPIDVFAILOLSYQFANTAAFGT----- 174
DB 133 -----LFVSRPAPRPGSGYVLRVAVNGT--TDLFVLTALV-----PPRGPHHP 174
OY 175 --YSKASCTRTGLPTVQLEALTRTESRMWQAYV--ATEATTTT-----AEATPTPV 224
DB 175 TPSSADECR-----PVV-----GSMHSLAVVPADAVFTTPPIPEPTTPAP 221
OY 225 TATSAS-----ELEAEHTFPWLENGVDHYEPTPANENSIVYRLGTSPTLIGYTA 277
DB 222 RGTGATPEPRSDDEEED-----EGATTAMTPVPGTLDANGTM--VUNASVSVRLV 271
OY 278 AVSATIG-----LVIVISIVTRNMCTPHKLDTVSODDEBSQTRRESRK 323
DB 272 AAANATGARGPGKIAMVIGPTIVLLIFLGVAACARCAARGIASTGRDPAARRSTR 331

RESULT 12
AAR80637
ID AAR80637 standard; Protein: 317 AA.
XX
XX AAR80637;
XX
XX 21-DEC-1995 (first entry)
XX
XX Bovine herpes virus-1 mutant ORF1 product.
XX
XX BHV-1; vaccine; gIV gene; antigen.
XX
XX Bovine herpesvirus.
XX
XX EP663403-A1.
XX
XX 19-JUL-1995.
XX
XX 18-NOV-1994; 94EP-0203361.
XX
XX 23-NOV-1993; 93EP-0203274.
XX
XX (ALKU ) AKZO NOBEL NV.
XX
XX Kell G;
XX
XX WPI: 1995-247499/33.
XX
XX N-PSDB: AAQ9001.
XX
XX New bovine herpes virus with mutation in ORF1 and polyA signal for
XX gIV gene - useful as a vaccine, esp. where the mutation is insertion
XX of sequence encoding an heterologous antigen
XX
XX Claim 2: Page 13-14; 28pp; English.
XX
XX To produce a new BHV-1 mutant, DNA encoding gIV (flanked on both
XX sides by a sequence that allows homologous recombination) and a
XX geotypically neg. BHV-1 (or its DNA) is introduced into a host
XX cell. Since the gIV neg. virus cannot replicate, virus particles
XX are produced only when homologous recombination with the DNA has

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XX 03-JUL-2001.
 PD 07-JUN-1995; 95US-0485289.
 XX 20-APR-1990; 90US-0513282.
 PR 21-JUN-1994; 94US-0262813.
 PR 28-AUG-1986; 86MO-US01761.
 PR 26-MAR-1986; 86US-0844113.
 PR 16-JUL-1986; 86US-0886260.
 PR 29-JUN-1987; 87US-0100817.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Petrovskis EA, Post LE, Timmins JG;
 PI WPI: 2001-432046/46.
 DR N-PSDB; AAF90626.
 XX New recombinant DNA for screening animals actively infected with
 PT pseudorabies virus (PRV), or for producing proteins useful as a vaccine
 PT for protecting animals against PRV infection
 XX Example 3; Column 21-24; 21pp; English.
 PS The present sequence is that of pseudorabies virus (PRV)
 CC glycoprotein gp53. The invention provides PRV gp50, gp63 and gI
 CC glycoproteins (see AAB82501-03) and polynucleotides (see
 CC AAF90625-27), and transformed host cells (especially CHO, yeast
 CC and Escherichia coli) used to produce the polypeptides. Also
 CC provided are subunit vaccines for PRV, methods for protecting
 CC animals against PRV infection and methods for distinguishing
 CC between infected and vaccinated animals. Commercial vaccine PRVs
 CC have been found to have the gI and gp63 genes deleted. The gI and
 CC gp63 polypeptides can therefore be used as diagnostic agents to
 CC distinguish between animals vaccinated with these commercial
 CC vaccines and those infected with the virulent virus.
 XX Sequence 350 AA:
 SQ
 Query Match 7.6%; Score 141.5; DB 22; Length 350;
 Best Local Similarity 22.8%; Pred. No. 3.7e-05;
 Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
 QY 8 LALLAATLAPFGAM--GIVTGNHVSARIDDDHIVAPREATIOLQLEFMPGQRPKRP 65
 DB 15 LLLAALLTLALTPRGVGLFRGAASVHAGSAVLPGDAPRLTIDGTLLEGPSPSN- 73
 Y 66 YSGTVARFRSDITNOCYQELSEERFENCSTRSSVFGCC--KTEYTFSSAS-----NRL 118
 DB 74 YSGRVGL-LRLDPKRCACRYREYAEDLCPRVHNEAFRCCLRKREPLARRASAAVEARBL 132
 QY 119 TGPPIPFKLTIRNPRDSCGMFYIVRLDQTKRPIQVFAIQLSYQFANTAAATRGU- 174
 DB 133 -----LFGSRPAPRPAAGSYVLRVAVNGT--TDLFVLTALV-----PRGRPHR 174
 QY 175 --YSKASCTFGLPTVOLEAVLRTESRMWMAVY--ATEATTTT-----AEATTPTPV 224
 DB 175 TSPSADCEK---PYV-----GSMHSLAVYVPADAVFTTPPIIEPEPTTPAPR 221
 QY 225 TATSAS-----ELEAHTFPPLNGVYHPTPAAANSVYRLQTSAPLLIGTYA 277
 DB 222 RCGCATPGRPSDEEBDE-----EGATTAATPVGTLIDANGTA--VLNAAVSIVL 271
 QY 278 AVVSATIG-----LTVISIVTRNMCIPKAKLDTYSQDDEESQTRRSKR 323
 DB 272 AAANAATAGARPGKITAMVGLPTIVYLLIFGVACARACANGIASTGDRGAARSTRR 331

RESULT 15
 AAR48063 standard; Protein: 380 AA.
 ID AAR48063
 XX

AC AAR48063;
 XX 20-JUL-1994 (first entry)
 DT Sequence of polypeptide encoded by the first open reading frame in
 DE the unique short (US) region of bovine herpes virus (BHV) genome.
 XX Insertion region; unique short region; US; vaccine; antigen.
 KW Bovine herpes virus type 1, strain ST.
 OS WO9400586-A.
 PN 06-JAN-1994.
 PD 25-JUN-1993; 93MO-FR00642.
 XX 26-JUN-1992; 92FR-0007930.
 XX (INMR) RHONE MERIEUX SA.
 PA Audoumet JF, Legastelois ICMA, Leung-tack P, Riviere MEA;
 PI WPI: 1994-026222/03.
 DR N-PSDB; AAO53350.
 DR New insertion region sequence of bovine herpes virus genomic DNA
 PT used for recombinant virus with this region deleted or
 PT inactivated, useful in vaccines allowing differentiation between
 PT vaccinated and infected cattle
 XX Claim 9; Fig 2; 47pp; French.
 PS The 1490 bp sequence in AAO53350 encodes polypeptides homologous to
 CC HSV-1 gI, gE and US9; these are neither essential for in vitro
 CC replication nor important in inducing a protective immune response.
 CC It is genomic DNA purified from the ST strain of BHV-1. (BHV is also
 CC known as infectious bovine rhinotracheitis virus.) The sequence
 CC forms the insertion region in genomic DNA. BHV in which the
 CC specific insertion region, esp. nucleotides 172-1311, has been
 CC deleted or inactivated by insertion are claimed.
 XX Sequence 380 AA:
 SQ
 Query Match 7.5%; Score 140.5; DB 15; Length 380;
 Best Local Similarity 25.3%; Pred. No. 5.2e-05;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;
 QY 1 MASLIGTIALIATLAPFGAMGIVTGNHVSARIDDDHIVAPREATIOLQLEFMP 58
 DB 1 MRCLIMVYVILARAP--ARSLVYRGEAVGLRADGVAVRHP--TDATLARGTLPLE 57
 QY 59 GORP-HRPSGTVARFRSDITNOCYQELSEERFENCSTRSSVFGCCKTEYTFSSASNR 117
 DB 58 HQLPAGRRVNGVEL-LRYHAAGDCFVMLQTTAFASCPRYANNAFSCLDHDTPRASER 116
 QY 118 LTGP--DHPKLTIRNPRDSCGMFYIVRLDQTKRPIQVFAIQLSYQFANTAAATRGU- 166
 DB 117 RASAAVNHVLEFIARPRIDSGVFLRVGIGYGTASERRRNVFLAFAVSGEGQDP 176
 QY 167 -----NTAATRGYKASCTFGL-----PTVOLEAVLRTESRM 201
 DB 177 EAARTAPRSQSRPASGLTSSALYRALARSPAPPPRPAARPAAGRRPERYDE 236
 QY 202 NMQAVVTEATTTSAATTPPTVYATSSAS 230
 DB 237 TTEVATRAGSAFALTPPAGPTASPA 265

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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:11:13 : Search time 19.5 Seconds
(without alignments)
546.210 Million cell updates/sec

Title: US-09-993-777-7
Perfect score: 1863
Sequence: 1 MASLGTALATLAPFGA.....VELVAIVPSALSSPSIKM 362

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5.

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AI.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1863	100.0	362	5	PCT-US96-03916-7	Sequence 7, Appl 1
2	1863	100.0	362	5	PCT-US96-03916-68	Sequence 68, Appl 1
3	152	9.2	355	4	US-08-709-731A-28	Sequence 28, Appl 1
4	148	7.9	317	2	US-08-344-833-2	Sequence 2, Appl 1
5	148	7.9	344	1	US-08-680-726A-56	Sequence 56, Appl 1
6	148	7.9	354	4	US-09-092-409-56	Sequence 10, Appl 1
7	145	7.7	310	3	US-08-911-321-10	Sequence 10, Appl 1
8	143.5	7.7	350	6	53525751-321-10	Sequence 10, Appl 1
9	140.5	7.5	360	4	US-08-924-345-2	Sequence 2, Appl 1
10	112	6.0	387	4	US-09-175-988-2	Sequence 2, Appl 1
11	108	5.8	713	1	US-08-190-802A-63	Sequence 63, Appl 1
12	108	5.8	713	4	US-08-477-346-63	Sequence 63, Appl 1
13	108	5.8	713	4	US-08-473-089-63	Sequence 63, Appl 1
14	108	5.8	713	4	US-08-487-072A-63	Sequence 63, Appl 1
15	108	5.8	713	4	US-09-108-857-3	Sequence 3, Appl 1
16	107.5	5.8	100	3	US-09-047-125-27	Sequence 27, Appl 1
17	107.5	5.8	100	3	US-07-736-335E-27	Sequence 27, Appl 1
18	103.5	5.6	94	1	US-08-150-203A-6	Sequence 6, Appl 1
19	103.5	5.6	94	1	US-08-454-730-6	Sequence 6, Appl 1
20	103.5	5.6	94	4	US-08-949-788-6	Sequence 6, Appl 1
21	99	5.3	97	3	US-09-047-125-25	Sequence 25, Appl 1
22	99	5.3	97	3	US-07-736-335E-25	Sequence 25, Appl 1
23	98	5.3	503	1	US-07-946-497-2	Sequence 2, Appl 1
24	98	5.3	503	1	US-08-483-322-2	Sequence 2, Appl 1
25	98	5.3	503	2	US-08-478-882-2	Sequence 2, Appl 1
26	97	5.2	1220	2	US-08-843-530B-36	Sequence 36, Appl 1
27	93.5	5.0	878	4	US-09-556-706B-2	Sequence 2, Appl 1

28	93.5	5.0	907	3	US-08-783-774-2	Sequence 2, Appl 1
29	93.5	5.0	907	4	US-09-328-599A-1	Sequence 1, Appl 1
30	93.5	5.0	907	5	PCT-US95-04611A-19	Sequence 19, Appl 1
31	92.5	5.0	547	1	US-08-314-615-1	Sequence 1, Appl 1
32	92.5	5.0	547	1	US-08-314-362-1	Sequence 1, Appl 1
33	92.5	5.0	547	1	US-08-433-010-1	Sequence 1, Appl 1
34	92.5	5.0	547	1	US-08-482-882-1	Sequence 1, Appl 1
35	92.5	5.0	547	2	US-08-483-389-1	Sequence 1, Appl 1
36	92.5	5.0	547	2	US-08-487-113D-1	Sequence 1, Appl 1
37	92.5	5.0	547	2	US-08-473-503-1	Sequence 1, Appl 1
38	92.5	5.0	547	2	US-08-483-932-1	Sequence 1, Appl 1
39	92.5	5.0	547	2	US-08-720-420A-1	Sequence 1, Appl 1
40	92.5	5.0	547	3	US-08-714-017-1	Sequence 1, Appl 1
41	92.5	5.0	547	3	US-08-863-790-1	Sequence 1, Appl 1
42	92.5	5.0	547	3	US-08-475-680-1	Sequence 1, Appl 1
43	92.5	5.0	547	4	US-08-296-749-1	Sequence 1, Appl 1
44	90.5	4.9	518	4	US-09-240-915-8	Sequence 8, Appl 1
45	90.5	4.9	518	4	US-09-591-435-8	Sequence 8, Appl 1

ALIGNMENTS

RESULT 1
PCT-US96-03916-7
Sequence 7, Application PC/TUS9603916
GENERAL INFORMATION:
Applicant: Wild, Martha A.
Applicant: Cochran, Mark A.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Cooper 8 Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-03916-7
Query Match 100.0%: Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%: Pred. 2, 5e-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MASLGTALATLAPFGAGMIVTGNHVSARIDDDHIVVAPRPATIQLOLFMPQ 60
1 MASLGTALATLAPFGAGMIVTGNHVSARIDDDHIVVAPRPATIQLOLFMPQ 60

QY 61 RPKPYSGIVAVAFRSDITNOCYOESEERFENCNTHRSSVFNCKVETESASNLTG 120
DB 61 RPKPYSGIVAVAFRSDITNOCYOESEERFENCNTHRSSVFNCKVETESASNLTG 120
QY 121 PPHFPLTINPNRPNDSGMFYVIRLDITKEPIDVFAIQLSVQFANTATRLGLYSASC 180
DB 121 PPHFPLTINPNRPNDSGMFYVIRLDITKEPIDVFAIQLSVQFANTATRLGLYSASC 180
QY 181 RTGGLPTVOLEAVLRTREESRNNQAVVATEATTSAEATTPPVATASASELAHEHTFP 240
DB 181 RTGGLPTVOLEAVLRTREESRNNQAVVATEATTSAEATTPPVATASASELAHEHTFP 240
QY 241 WLENGVDHEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
DB 241 WLENGVDHEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
QY 301 HRKLDIVSODDERSQTRRSRKFPGPVACEINKGADQDSELEVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDERSQTRRSRKFPGPVACEINKGADQDSELEVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 2

PCT-US96-03916-68

Sequence 68, Application PC/TUS9603916

GENERAL INFORMATION:

APPLICANT: Wild, Martha A.

APPLICANT: Cochran, Mark D.

TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/03916

FILING DATE: 23-MAR-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/126,597

FILING DATE: 24-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 39116-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 362 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-03916-68

Query Match 100.0%; Score 1863; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.5e-188;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASLGLTALLAATLAPFGAMGIVITGNHVSANRIDDHIVIVAPREPATIQQLFFMPGQ 60
DB 1 MASLGLTALLAATLAPFGAMGIVITGNHVSANRIDDHIVIVAPREPATIQQLFFMPGQ 60
QY 61 RPKPYSGIVAVAFRSDITNOCYOESEERFENCNTHRSSVFNCKVETESASNLTG 120
DB 61 RPKPYSGIVAVAFRSDITNOCYOESEERFENCNTHRSSVFNCKVETESASNLTG 120
QY 121 PPHFPLTINPNRPNDSGMFYVIRLDITKEPIDVFAIQLSVQFANTATRLGLYSASC 180
DB 121 PPHFPLTINPNRPNDSGMFYVIRLDITKEPIDVFAIQLSVQFANTATRLGLYSASC 180
QY 181 RTGGLPTVOLEAVLRTREESRNNQAVVATEATTSAEATTPPVATASASELAHEHTFP 240
DB 181 RTGGLPTVOLEAVLRTREESRNNQAVVATEATTSAEATTPPVATASASELAHEHTFP 240
QY 241 WLENGVDHEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
DB 241 WLENGVDHEPTPANENSNTVRLGTMSPLIGVTAAVVSAITGLIVISITVRNKCPT 300
QY 301 HRKLDIVSODDERSQTRRSRKFPGPVACEINKGADQDSELEVAIVNPSALSSPDSI 360
DB 301 HRKLDIVSODDERSQTRRSRKFPGPVACEINKGADQDSELEVAIVNPSALSSPDSI 360
QY 361 KM 362
DB 361 KM 362

RESULT 3

US-08-709-731A-28

Sequence 28, Application US/08709731A

Patent No. 6322780

GENERAL INFORMATION:

APPLICANT: Lee, Lucy F.

APPLICANT: Nazerian, Keyvan

APPLICANT: Witter, Richard L.

APPLICANT: Wu, Ping

APPLICANT: Yanagida, No. 6322780oru

TITLE OF INVENTION: Marek's Disease Virus Genes and Their

TITLE OF INVENTION: Use in Vaccines for Protection Against Marek's Disease

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch and Birch, LLP

STREET: P.O. Box 747

CITY: Falls Church

STATE: VA

COUNTRY: US

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,731A

FILING DATE: 05-JUL-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/499,474

FILING DATE: 07-JULY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1644-110FPC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acid

STRANDNESS: not relevant

TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE: internal
 ORGANISM: Marek's disease virus type I
 STRAIN: GA
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..353
 OTHER INFORMATION: /label= protein
 OTHER INFORMATION: /note= 'g1 protein'
 US-08-709-731A-28

Query Match 8.2%; Score 152; DB 4; Length 355;
 Best Local Similarity 22.9%; Pred. No. 1.2e-07;
 Matches 78; Conservative 55; Mismatches 166; Indels 42; Gaps 14;

19 GAMGIVITGNHVSARIDDDHIVIVAPRPE-ATIQQLFPMGQPHKPYSGIVAVAFKSD 77
 15 GIMSVIVTGTSTLTSDQSALVAFGGLDMVNVKQQLLEGGDRTSTGTTEL-LKMD 73
 78 ITNOCYOEISEERENCNTHRSSVFVGCCKVTEYTFASNRLLTGPPEFK--LITRNP 134
 74 EEKCYSLVHATSYMDCPAIDATVFRGCDAAVVAQPHDRV--QPEPEKGLLRIVERPV 131
 135 NDSGMYVIVRLDTPKEPIDVFAIQLSYQFANFATRGVSKASCKTEGLPTVQLEAVL 194
 132 SDTGSYIVFVALAG-RNMSDIFRMVAVIRS-----SKSMACHSASFQAHNCI 179
 195 RTEE--SMENQAVVATEATTTSEATTPPTVATASASELAEHFTFPMLENGVDHYEPT 252
 180 RYVDRMAFENYLIQHVGLDSDSELHAIYINITPOSIS-TDINIITTFPDNSGTLTSP 238
 253 P--ANENSNVRLGT-MSPTLIGVVAAY--SATIGLVV---TSIVTRMCTPHRK 303
 239 VFMLFNHNVHDMANSTGMNTVLYKTLPELTYFSMLVLCIALIAYLVCERCGRSPHRR 298
 304 LDTVSODDEESQTRRESKRGKPVVACEINKGADODSEIVE 344
 299 I-----YIGPRSD-----APLITSANVESPOVDYANKE 328

RESULT 4
 US-08-344-833-2
 Sequence 2, Application US/08344833
 Patent No. 5874280
 APPLICANT: Kell, G. ether
 TITLE OF INVENTION: Recombinant Bovine Herpesvirus
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Organon Teknika Corporation
 STREET: 1330-A Piccard Drive
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/344,833
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Blackstone, William B.
 REGISTRATION NUMBER: 29,772
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 258-5200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-344-833-2

Query Match 7.9%; Score 148; DB 2; Length 317;
 Best Local Similarity 27.1%; Pred. No. 2.7e-07;
 Matches 68; Conservative 34; Mismatches 125; Indels 24; Gaps 11;

1 MASLGTALAAATLAFPGAMGIVITGNHVSARIDDDHIVIVAPREATQI--OLFMP 58
 1 MRRLLMMVVLAAABP--ARSLVYRGEAVNGIRADGPAVAVHP-TDATALRGLTLE 57
 59 GGRP-HKPYSGTVAVAFRSDITNOCYOEISEERENCNTHRSSVFVGCCKVTEYTFASNR 117
 58 HQLPAGRRYNGTVEL-LRYHAAGDCFVMLQTAFAFASCPVANDAFRSCUHADTRPARSER 116
 118 LTGP--PHPEKLTIRNRPNDSCMFYIVRL---DQKEPIDVFAIQLSYQFAN--- 167
 117 RASAAVENHVLSTARBRPIDSGLYFLRVGIVGTAGSERRRDVFPLAIVHSFGEPGD 176
 168 --TAATRGVYS--KASCRFGPLTVQLEAYLTREESMNMQAVVATEATTSATPTPT 223
 177 EAAAHFPGVVEAVERCER-GLDASSASLYDALAAFPAGAA--TPGPTASSSGAATP 233
 224 VTATASLEEA 234
 234 ERYDETTEVEA 244

RESULT 5
 US-08-680-726A-56
 Sequence 56, Application US/08680726A
 Patent No. 5804197
 APPLICANT: Haanes, Elizabeth J.
 TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
 NUMBER OF SEQUENCES: 92
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross & McIntosh
 STREET: 1700 Lincoln Street, Suite 3500
 CITY: Denver
 STATE: Colorado
 COUNTRY: U.S.A.
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/680,726A
 FILING DATE: 12-JUL-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Connell, Gary J.
 REGISTRATION NUMBER: 32,020
 REFERENCE/DOCKET NUMBER: 2618-46-C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-680-726A-56

Query Match 7.98; Score 148; DB 1; Length 364;
Best Local Similarity 27.38; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

4 LGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREATTQLOLFMPGQR-P 62
16 LITMFLPIFLFLYNGVYKGTYSMLNSSGFSIFPDDKFIYSGRLFLDDHLS 75
63 HKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSVEVC--KVTEYFASNRITG 120
76 VNNVSGTIEFI--HFNNCTVYQTEIEFSCPRIFNNAFSCCLKKYSKHHSQLRINSS 132
121 PPHPKLTINRPNDSGMFYIVRLDDTKEPIDVFAIQLSVQF 165
133 IENGVLLEITNPKPNDGCVFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 6

US-09-092-409-56

Sequence 56, Application US/09092409

Patent No. 6159478

GENERAL INFORMATION:

APPLICANT: Haanes, Elizabeth J.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
City: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-092-409-56

Query Match 7.98; Score 148; DB 4; Length 364;
Best Local Similarity 27.38; Pred. No. 3.3e-07;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

4 LGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREATTQLOLFMPGQR-P 62
16 LITMFLPIFLFLYNGVYKGTYSMLNSSGFSIFPDDKFIYSGRLFLDDHLS 75
63 HKPYSGTVRAFRSDITNOCYQELSEERFENCSTRSSVEVC--KVTEYFASNRITG 120
76 VNNVSGTIEFI--HFNNCTVYQTEIEFSCPRIFNNAFSCCLKKYSKHHSQLRINSS 132

121 PPHPKLTINRPNDSGMFYIVRLDDTKEPIDVFAIQLSVQF 165
133 IENGVLLEITNPKPNDGCVFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 7

US-08-911-321-10

Sequence 10, Application US/08911321

Patent No. 6010703

GENERAL INFORMATION:

APPLICANT: Roger K. Maes and Stephen J. Spatz
TITLE OF INVENTION: Recombinant Poxvirus
TITLE OF INVENTION: Vaccine Against
TITLE OF INVENTION: Feline Rhinotracheitis
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
City: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,321
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/096,183
FILING DATE: July 26, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 6010703e
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 370
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Feline herpesvirus-1
STRAIN: 1
INDIVIDUAL ISOLATE: C-27
CELL TYPE: N/A
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: Deduced Sequence
OTHER INFORMATION: 91
US-08-911-321-10

Query Match 7.88; Score 145; DB 3; Length 370;
Best Local Similarity 22.08; Pred. No. 7.1e-07;
Matches 72; Conservative 52; Mismatches 136; Indels 68; Gaps 14;

5 LGTLLAATLAPFGAMGIVITGNHVSARIDDDHIVAPRE-ATTQLOLFMPGQR-RP 62
1 MSIAFIYILMAIGTYGIVYGRDHDVSLHVDTSAGFYIYTLLENFTLYGHLIFLDDQPLP 60

RESULT 10
US-09-175-928-2
Sequence 2, Application US/09175928A
Patent No. 6312921
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racle, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Mi, Sha
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION NUMBER: US/09/175,928A
CURRENT FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 387
TYPE: prt
ORGANISM: Homo sapiens
US-09-175-928-2

Query Match
Best Local Similarity 19.2%; Pred. No. 0.0023;
Matches 77; Conservative 58; Mismatches 129; Indels 138; Gaps 20;

6.0%; Score 112; DB 4; Length 387;
Best Local Similarity 19.2%; Pred. No. 0.0023;
Matches 77; Conservative 58; Mismatches 129; Indels 138; Gaps 20;

1 MASLCTLLALLAATLAPFGAMGIVITGNHVSARIDDDHIVAPREPATQQLFFMPGQ 60
12 LSLAQSVSVOYTI-PDGFVNVTGSMNLTLCI---YTTVASRQLSTIOMSEFF----- 62
61 RPKRYSGYRVAFRSDITNQCQELSEERFENCSTRSSVPFGCAVTEFTFSASRLTG 120
63 --HKKEPEPSTIF-----SOGGQVAIG-----OFKDRITG 92
121 PPHF--FKLIRNRPNDGSMFYIVRLDTPKEIDVFAIQLSVYFANTATRGILYSKA 178
93 SNDFGNASTISHMOPADSGIY-----ICDVNPNPDLGQNGILNVSIVLKP-----SKP 143
179 SCRTFLP---TVLEAVIKRTESWRNMQAVATETATTSATATPTPTATASLELA 234
144 LCSVQGRPEPTGHTISLSCL-----SALGTPSPV-----RLG----- 171
235 EHTEFMLENGVDHYEPTPANENSNTV-----RLG----- 265
172 ----YTW--HKLEGRIVPEKEMENPTTGLVIGNLTNPEQGYOCTAINRLNLSCEID 225
266 -TWSPPLIGVTAAYVASATIGLVISIVTRNNCTPHRLDLTVSODDEERSQTRRESRKP 324
226 LTFSSHEVGIIIGALIGLGAIIISVY---CFARNKAKAKAK--ERNSKTIAE---L 276
325 GPRVACEINKGADODS---ELVELVAIVNPSAL--SSPSISK 361
277 EPMT--KINPRGESEAMPREDATQLEVTLPSSIHETGPDTIQ 316

RESULT 11
US-08-190-802A-63
Sequence 63, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dellinger & Associates
STREET: P.O. Box 60850

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TUPL, Fig. 46
US-08-190-802A-63

Query Match
Best Local Similarity 5.8%; Score 108; DB 1; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

5.8%; Score 108; DB 1; Length 713;
Best Local Similarity 27.3%; Pred. No. 0.016;
Matches 62; Conservative 30; Mismatches 89; Indels 46; Gaps 11;

60 QRPKRYSGYRVAFRSDITNQCQELSEERFENCSTRSSVPFGCAVTEFTFSASRLTG 115
86 QRDHQLASLTVLQD 144
116 NRTGPPHPEKLTIRNRPNDGSMFYIVRLDTPKEI-----D 154
145 NTTGSPSAF--PVQASRLVGS-----QLPTTLPVYSNNQQLPQQLDQDQDQDQDQ 197
155 VFAIQLSVYOFANATATRGILYSKASCTRGFLPTVQI--EAVLRTESWRNMQAVV-----A 208
198 QPPQVSAVPLSNTAING---SPTSKETTLPLPSVKAPESTLKETPEENNNTSKINDGSA 254
209 TEATTSAEAT--TPPTVATASLEAEHTEFPMLENGVDHYEPTP 253
255 TVATTTATETETKPEEDATPAS-LHODHYLVIPNOR-ANHSKPIP 295

RESULT 12
US-08-477-346-63
Sequence 63, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:09:18 ; Search time 15.5 Seconds

(without alignments)
2245.204 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1663

Sequence: 1 MASLGLTALALATAPRGA.....VELVAVNPMSALSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	164	8.9	420	2 T42616	envelope protein -
2	162.5	8.7	354	1 VGBE67	glycoprotein D pre
3	153	8.3	353	1 C46113	glycoprotein D pre
4	153.5	8.2	424	1 VGBE63	glycoprotein gp63
5	143.5	7.7	350	1 VGBE63	glycoprotein gp63
6	140.5	7.5	380	2 S33785	glycoprotein I - b
7	125	6.7	356	2 J02352	glycoprotein I - t
8	124.5	6.7	683	2 T03146	probable glycoprot
9	115	6.2	457	1 RNMST4	cell surface gly
10	113.5	6.1	390	1 ODBE77	glycoprotein I pre
11	111.5	6.0	149	2 A61162	glycoprotein I pre
12	108.5	5.8	355	2 C39725	hypothetical prote
13	108	5.8	713	2 JN0133	WD-40 repeat regul
14	107	5.7	372	1 ODBE88	glycoprotein I pre
15	99	5.3	372	1 R3674	glycoprotein I pre
16	99	5.3	1036	2 S73601	glycoprotein I pre
17	98.5	5.3	1140	2 S73786	glycoprotein I pre
18	98	5.3	503	2 B38745	cell adhesion mole
19	98	5.3	507	2 S64507	probable membrane
20	97	5.2	1220	2 S48387	SN1 protein - yea
21	96.5	5.2	814	2 A39752	fibroblast growth
22	95.5	5.1	797	1 VGBEX1	glycoprotein X pre
23	95.5	5.1	867	2 T45463	membrane glycoprot
24	95	5.1	1777	2 T43469	hypothetical prote
25	94	5.0	796	2 T21460	hypothetical prote
26	93.5	5.0	645	2 T29818	hypothetical prote
27	93.5	5.0	907	1 ODBE21	membrane antigen g
28	93	5.0	3020	2 A43932	mucin 2 precursor,
29	93	5.0	1051	2 S55259	TfPI protein - mou

30	92.5	5.0	1778	2 AF1116	internalin protein
31	92	4.9	1044	2 P65375	probable drug resi
32	91.5	4.8	510	2 T47374	hypothetical prote
33	91	4.8	365	2 A34424	Cd64 membrane gly
34	91	4.8	836	2 S49940	cell division cont
35	90.5	4.9	836	2 S28904	intercellular adhe
36	90.5	4.9	785	2 T37329	probable oligopept
37	90.5	4.9	786	2 T19017	hypothetical prote
38	90.5	4.9	1429	2 T41699	C2-domain family P
39	90	4.8	233	2 C84193	hypothetical prote
40	90	4.8	798	2 T34248	hypothetical prote
41	89.5	4.8	826	2 G90283	hypothetical prote
42	89.5	4.8	866	2 T45462	membrane glycoprot
43	89.5	4.8	929	2 T38817	hypothetical prote
44	89	4.8	629	2 AE1525	probable peptidog
45	89	4.8	678	2 S54308	DNA binding protei

ALIGNMENTS

RESULT 1	T42616	envelope protein - equine herpesvirus 4 (strain NS80567)
C:Species: equine herpesvirus 4	A:Variety: strain NS80567	C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42616	R:RefSeq: E. A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.	J. Gen. Virol. 79, 1197-1203, 1998
A:Title: The DNA sequence of equine herpesvirus-4.	A:Reference number: Z22173; MUID:98264497; PMID:9603335	A:Note: The DNA sequence of equine herpesvirus-4.
A:Accession: T42616	A:Status: preliminary; translated from GB/EMBL/DBJ	A:Residues: 1-420 <REP>
A:Note: 73	C:Genetics:	A:Experimental source: strain NS80567
C:Superfamily: pseudorabies virus glycoprotein gp63		
Query Match	8.8%	Score 164; DB 2; Length 420;
Best Local Similarity	25.5%	Pred. No. 9.6e-06;
Matches	96; Conservative	50; Mismatches 143; Indels 88; Gaps 21;
OY	10	LLAATLAPGAMGIVITGNHVSARIDDDHIVAPPEATLQ-OLFFMGQR-PKPKPS 67
DB	13	LIAISMCM--ATAIYRGHMSMTLNSSEFAVYPRKSLVVGMLFDGQRLPTTNS 69
OY	68	GTVVAFRRSDITWOCYQELSEERFECTHRSSVFVGC--KVTEYTESASRLTGPPHP 125
DB	70	GLIEL-IHNYSHGCVSYQITISYESCPRVANNAFRSCLAKTSNHNODYFHVNTSVETNV 128
OY	126	KLTFRNRPDSDGMEFYVIRLDDTKEPIDVFAIQLSVQF-ANTATRGLYSKASCTRG 184
DB	129	LLNTRPOPDSQATYILRVKLNHA-PTADVFGSAFVYDQSNVPEVPYPAKPPSNVET 187
OY	165	LPTVOLAFVYRTESNRNOAVATEATTSABEAT--TPPTVTATASASELAHETFEW 241
DB	188	RTAPAPANSTR-----TGSNNTSSOSTWLYLPTP-----RPA 221
OY	242	LENGVDHKEPTPANEN--SNVTVRL-----GTMSFP-----LIGVVAVVSATIG---- 285
DB	222	LEF---HLITRANPEVVSQGTAMLCHEFRSTAVPTIYMHLLGLT-----GWLPE 269
OY	286	-LVIVISITRMMCKPHKLDTS-----ODDESRQTPREAR-KFQPVN-----ACEIN 333
DB	270	DVLLEDESELR---TPPKPOTISSRTGDDFGQNTSTSPKSNKIVAMVIVTACVLM 326
OY	334	KGADQSEVELVAVYN 350
DB	327	-----LLLVVGGIIN 337

RESULT 2

VGBE67

glycoprotein D precursor - human herpesvirus 3

N:Alternate names: glycoprotein IV

C:Species: human herpesvirus 3, varicella-zoster virus

C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999

C:Accession: F27345

R:Davidson, A.J.; Scott, J.E.

J. Gen. Virol. 67, 1759-1816, 1986

A:Title: The complete DNA sequence of varicella-zoster virus.

A:Reference number: A27345; MUID:86306657; PMID:3018124

A:Accession: F27345

A:Molecule type: DNA

A:Residues: 1-354 <DAV>

A:Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27950.1; PID:g60056

C:Genetics:

A:Superfamily: herpesvirus glycoprotein D

Keywords: glycoprotein; phosphoprotein; transmembrane protein

-17/Domain: signal sequence #status predicted <SIG>

F:279-295/Domain: transmembrane #status predicted <TMN>

F:33,47,67,116/Binding site: carbohydrate (Asn) (covalent) #status predicted:

Query Match 8.7%; Score 162.5; DB 1; Length 354;
 Best Local Similarity 22.4%; Pred. No. 1e-05;
 Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

QY 23 IVTGNHVSARIDDDHIVAPPRE--ATIQQLFFMPQRP-HKPYSGTVARFSDI 78
 DB 21 LIRKGVHVSQVNSSLTSLIPQNDNYTEIKQLVIGQLPTGNYSGTELLLY-ADR 79
 79 TNCYOELSEERENCNHRSSVFGCKV--EYTFASNRLLGPHPRKLTIRNRPN 135
 DB 80 VACFSSVOYIRIDGCPRTITSAFISCRKHSNHYGNDSTRIBPDAGWMLITPKGIN 139
 QY 136 DSGMFYVIRLDDTKEPIDVFIQLSVY-----QFANTAATGLYSKAS 179
 DB 140 DACVYVLLVRLDHSRS-TDGFILGVNVYTAGSHNHNGVITSPSLONGYSTALFQQA- 197
 QY 180 CRFFGLPT-----VQLEAVLRTEES-WRMQAVVATEATTSAETTPRPV 225
 DB 198 -RIGCDIPAPPKGSGTSLFQMLDLRAGKSLDNPWLH-EDVVTETKRSVYKEG----- 248
 QY 226 ATASELEAHEFTFPMLENCVDHYEPTPAN---ENS-----NVTVRLGTMSPTLIGTV 276
 DB 249 -----IEN---HYVPTDMSTLEPKSLNDPEMLLT-----IIPVA 281
 DB 277 AAVVSATIGLVIVISIVTRNM 297
 DB 282 SVMILTAMVIVIVISVKKRRI 302

RESULT 3

C46113

glycoprotein D precursor - cercopithecine herpesvirus 9 (strain DHV)

N:Alternate names: membrane glycoprotein 1

C:Species: cercopithecine herpesvirus 9

C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999

C:Accession: C46113

R:Fletcher III, T.M.; Gray, W.L.

Virology 193, 762-773, 1993

A:Title: DNA sequence and genetic organization of the unique short (Us) region of the st

A:Reference number: A46113; MUID:93312509; PMID:8384754

A:Accession: C46113

A:Molecule type: DNA

A:Residues: 1-353 <FLE>

A:Cross-references: GB:I07067; NID:g310715; PIDN:AAA47888.1; PID:g310718

C:Superfamily: herpesvirus glycoprotein D

C:Keywords: glycoprotein; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-353/Product: glycoprotein D #status predicted <GPD>
 F:275-293/Domain: transmembrane #status predicted <TMN>
 F:40,75,84,122,138,227,252/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 8.3%; Score 155; DB 1; Length 353;
 Best Local Similarity 20.2%; Pred. No. 4.2e-05;
 Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11;

QY 18 FG---AMGIVITGNHVSARIDDD--HIVAPPREATIQQLFFMPQRP-HKPYSGTV 71
 DB 20 FGIOCAAIIRNYISLYVNSATSLFGLGNNDASIRGRFLFIDGQFVTNTYNTVE 79
 QY 72 VAFRSIDTNCYOELSEERENCNHRSSVFGCKV--EYTFASNRLLGPHPRKLTIR 130
 DB 80 L-LHVNOTTLQPLVRYVMGECPRITRTGAILICRYRSHVYENAOQLDPNVEIIFKMN 138
 QY 131 NRPNSGMYVIRLDDTKEPIDVFIQLSVYQFANTAATRLGLSKASRTGGLPYOL 190
 DB 139 NTVVEDAGIYLLVQLDYT-SLPDIFPVSLNVPKQDTSMEDVY-----FPEVYS 188
 QY 191 EAV-LRTEESMRMQAVVATEATTSAETTPRPVATSAELEAHEFTFPMLENCVDHY 249
 DB 189 PSHILNFKIKCHFPVHNGEOSTLCHIV-----SDVDTERENLSMKDLDGSR 238
 QY 250 EPPANENSNTVYRL-----GTMSPTLIGTVAAVVSATIGLVIVISIVTRNMC 298
 DB 239 QKPRKNFNPVKVNVTHETRTKLTMESSADVEMIAVPTASLVLAILIIVTVGIYRRRS 298
 QY 299 TPRKIDTVSODDEENSGTRRE 320
 DB 299 SEKRKIYPRKTRKQASTERE 320

RESULT 4

VGBE9

glycoprotein gp63 precursor - equine herpesvirus 1

N:Alternate names: glycoprotein I precursor; hypothetical 46k protein; ORF2 protein

C:Species: equine herpesvirus 1

A:Note: host Equus caballus (domestic horse)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: C36646; J00998; A36803

R:Audonnet, J.C.; Winslow, J.; Allen, G.; Paoletti, E.

J. Gen. Virol. 71, 2969-2978, 1990

A:Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with h

A:Reference number: A36646; MUID:91108393; PMID:2177089

A:Accession: C36646

A:Molecule type: DNA

A:Residues: 1-424 <ND>

A:Cross-references: GB:M6664; NID:g330791; PIDN:AA802508.1; PID:g330864

A:Experimental source: strain Kentucky D

R:Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, W.A.

Gene 101, 203-208, 1991

A:Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine herpesvir

A:Reference number: J00998; MUID:91276272; PMID:1647359

A:Accession: J00998

A:Molecule type: DNA

A:Residues: 1-424 <ELT>

A:Cross-references: GB:M6664; NID:g330787; PIDN:AAA6547.1; PID:g330788

R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.

submitted to GenBank, March 1992

A:Description: The DNA sequence of equine herpesvirus-1.

A:Reference number: A36803

A:Accession: A36803

A:Molecule type: DNA

A:Residues: 1-424 <TEL>

A:Cross-references: GB:M6664; NID:g330791; PIDN:AA802508.1; PID:g330864

A:Experimental source: strain Ab4P

R:Teiford, E.A.R.; Watson, M.S.; McBride, K.; Davidson, A.J.

Virology 189, 304-316, 1992

A:Title: The DNA sequence of equine herpesvirus-1.

A:Reference number: A41831; MUID:92295566; PMID:1318606

A:Contents: annotation; possible protein-coding frames

A:Note: neither amino acid nor nucleotide sequence is given

C:Genetics:

A:Gene: 73

C:Superfamily: pseudorabies virus glycoprotein gp63

C:Keywords: glycoprotein; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-44/Domain: glycoprotein gp63 #status predicted <MNT>

F:330-336/Domain: transmembrane #status predicted <TM1>

F:35,67,78,121,131,236,307/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

8.2%; Score 153.5; DB 1; Length 424;

Best Local Similarity 23.8%; Pred. No. 7.1e-05;

Matches 70; Conservative 41; Mismatches 126; Indels 57; Gaps 12;

QY 1 MASLIGTLLAATLAPFGAMGIVTGNHVSARIDDDHIVAPREATTIOL-QLEFMDG 59
 DB 1 MARLTFMSALLISMAICSAITRIYREHNSMYLANSSEFAVYPLDQSLVIGHLLFLDG 60
 QY 60 QR-PKRYSGTVAVAFRSDITNOCYQELSEERENTHSSSVFVGC--KYTEYTFSSAN 116
 61 QRLPTNLSGIEL-IHIVSSVCYVIGIOTISYSCPRVANNARFSLCKHYSKHVDYFR 119
 QY 117 RLTPRPPEKLTIRNPRPDSGMFYVIRLDDEKEIDVEATQLSVQFANTATGLYS 176
 DB 120 VNASVETNVLNITKPOPLDSQATILKYLKIDHA-PRADYGVSAVYDL----- 167
 QY 177 KASCRTEGLPTVQ---LEAYRTRESKRMKQAVATETTTT---AATPTPTATSA 229
 DB 168 KSKIVPDPMPPTQTVEPTTSYVSTPTDYDDVTEETESTISTQOAMTSTQTP-SATWG 226
 QY 230 SELAEHFTFPWLENGVDHYEPTPANENSNTVRLG-----TMSPTL 271
 DB 227 TQLTYE-----LPTNE---TVVIGQELLCMHFQPTSTVPTL 260

RESULT 5

VGBE63

glycoprotein gp63 - suid herpesvirus 1

C:Species: suid herpesvirus 1

A:Note: host sus scrofa domestica (domestic pig)

C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jul-1999

C:Accession: A29012

R:Petkovskis, E.A.; Timmins, J.G.; Post, L.E.

J. Virol. 60, 185-193, 1986

A:Title: Use of lambda-phage to isolate genes for two pseudorabies virus glycoproteins

A:Reference number: A93021; MID:86308235; PMID:3018284

A:Accession: A29012

Molecule type: DNA

Cross-references: GB:M14336; NID:9334055; PIDN:AMC35204.1; PID:9334056

A:Experimental source: strain Rice

C:Superfamily: pseudorabies virus glycoprotein gp63

C:Keywords: glycoprotein; transmembrane protein

F:11-27/Domain: transmembrane #status predicted <TM1>

F:286-308/Domain: transmembrane #status predicted <TM2>

F:56,73,153,256,262,275/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

7.7%; Score 143.5; DB 1; Length 350;

Best Local Similarity 22.8%; Pred. No. 0.00037;

Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;

QY 8 LALLAATLAPFGAM--GIVTGNHVSARIDDDHIVAPREATTIOLQLEFMDGPRPKP 65
 DB 15 LALLAATLAPFGAM--GIVTGNHVSARIDDDHIVAPREATTIOLQLEFMDGPRPKP 73
 QY 66 YSGTVAVAFRSDITNOCYQELSEERFENTHSSSVFVGC--KYTEYTFSSAS-----NRL 118
 DB 74 YSGTVAVAFRSDITNOCYQELSEERFENTHSSSVFVGC--KYTEYTFSSAS-----NRL 132
 QY 119 TGRPHPKLTIRNPRPDSGMFYVIRLDDEKEIDVEATQLSVQFANTATGLY----- 174
 DB 133 -----LFSNRPAPRDSGIVLRYVNGT---TDLFVLTALV-----PRGSRPHR 174
 QY 175 --YSKASCRTEGLPTVQLEAYRTRESKRMKQAV--ATEATTTT-----AATPTPTATSA 224

Db

175

TPSSADECR-----FVV-----GSMHDSLRVDDPAEDAVTTPPILEPEPTTAPP 221

QY

225

TATSSA-----ELEAEHFTFPWLENGVDHYEPTPANENSNTVRLGTMSPFLIGTVA 277

Db

222

RCIGATPEPRSDDEDEDE-----EGATTAMTPVPGTLNACTM--VLANSVSVRL 271

QY

278

AVVSATIG-----LVIVISIVTRNMCTPHRKLDIVSODDENSOJTRRESRK 323

Db

272

AANATAGARCGKIAMVIGPTIVLLIFLGVACARCARCIASGTGHDPGARRSTR 331

RESULT 6

S35785

glycoprotein I - bovine herpesvirus 1

C:Species: bovine herpesvirus 1

C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 24-Nov-1999

C:Accession: S35785

R:Audonnet, J.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35782

A:Accession: S35785

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-380 (AUD)

A:Cross-references: EMBL:Z23068; NID:9312185; PIDN:CAAB0605.1; PID:9312189

C:Superfamily: pseudorabies virus glycoprotein gp63

C:Keywords: glycoprotein

Query Match

7.5%; Score 140.5; DB 2; Length 380;

Best Local Similarity 25.3%; Pred. No. 0.00072; Indels 43; Gaps 9;

Matches 68; Conservative 33; Mismatches 125;

QY 1 MASLIGTLLAATLAPFGAMGIVTGNHVSARIDDDHIVAPREATTIOL-QLEFMDG 59
 DB 1 MRCLLMVWVLAARAP--ARSLVRCGAVGLRDRGPAFAVHP-TDVTALRQRLIFLE 57
 QY 59 GORP-HKPYSGTVAVAFRSDITNOCYQELSEERFENTHSSSVFVGCKYVEYTFSSANR 117
 DB 58 HOLPARGRYNGYEL-LFYHAAGDFVMLQTTAFASCPFRVANNARFSLCKHYSKHVDYFR 116
 QY 118 LTGP--PHPKLTIRNPRPDSGMFYVIRLDDEKEIDVEATQLSVQFANTATGLY----- 166
 DB 117 RASAANVNHVFLSARPRIDSGILFELVGIYGTAGSERRDVPLAFAVHSPGEGDP 176
 QY 167 -----NTATRGLYSKASCRTEGL-----PTVQLEAYLTRESMR 201
 DB 177 EAAATPAPRSQSPASGLTSASLYDRALARSPQAPPPRPAAPAAACGRRPERVDE 236
 QY 202 NMQAVVATEATTSAEATTPPYVATSSAS 230
 DB 237 TTEVAAATRAGSAPALTTPPAGPTASPA 265

RESULT 7

J02352

glycoprotein I - turkey herpesvirus

N:Alternate names: ORF 7 protein

C:Species: turkey herpesvirus

C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999

C:Accession: J02352

R:Zeinuk, V.; Bartell, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ro

J. Gen. Virol. 74, 2151-2162, 1993

A:Title: The complete sequence and gene organization of the short unique region of he

A:Reference number: J02346; MID:94014999; PMID:8409940

A:Accession: J02352

Molecule type: DNA

A:Residues: 1-356 (ZEL)

C:Keywords: glycoprotein; transmembrane protein

F:5-21/Domain: transmembrane #status predicted <TM1>

F:277-293/Domain: transmembrane #status predicted <TM2>

F:154,167,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:35-114/Domain: immunoglobulin homology <IM1>
F:139-190/Domain: immunoglobulin homology #status atypical <IM2>
F:230-301/Domain: immunoglobulin homology <IM3>
F:241-457/Product: Cyt, brain-specific short form #status predicted

F:321-372/Domain: immunoglobulin homology <IM4>
F:395-419/Domain: transmembrane #status predicted <TM>
F:420-457/Domain: intracellular #status predicted <INT>
F:42-112,159-188,328-370/Dsulfide bonds: #status predicted
F:187,298,332,392/Binding site: carbohydrate.(Asn) (covalent) #status predicted

Query Match 6.2%; Score 115; DB 1; Length 457;
Best Local Similarity 20.6%; Pred. No. 0.11;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

OY 19 GAAGVITNHNHSAIDDDHIIVAPRENTIOLQF---EMPGRPHKPGSGTVAR 75
Db 93 GSPELII--NKIKMRDSOTYICELENRKE-EVELWFKVTSPGSLIQOSLTLLDLSN 149
OY 76 SDITTCYOELSEEFENCCTRRSSSVFGCKVTEYTFASNNLRTPHPHEKLIRNRP 135
Db 150 SKYSN-----PLTE-----CKHKRGKVVGSKV-----LSKSNLRQ 181
OY 136 DSGMFVIYRLDTEPIDVEAIALSVQEPANTATRLGLYSKASCRTFLPTVOLEAYIR 195
Db 182 DSFPNMCYTALLOCK---NMFGMTLVLGFOSTAIT-AVKSGBESAEPSLFNAE---- 233
OY 196 TEESWRN--WQAVYVATEATTTSABATPTPTVATSASELAHEFTFPLENGVDHEPPT 253
Db 224 -ENMGELMKKA-----EKSFQPMISSTINKKEYS 265
OY 254 ANENSNTVATLGTMSPTLIGTVAVAVSATIGLVISIVTRNMCTPIRKLDIVSQDEE 313
Db 266 OKSTRDKIOLKETTELTKLPQLQSLOPASGNL---TLTIIDKGILQEVNLVVMKVAQ 321
OY 314 RSQTRRESRKFGPMACEIN-----KGADD---SELVELVAIWPSA----- 353
Db 322 LNNP-----LCCEVMGFSPKRMRLTKQEDCARVSEOKVQVAVAPETGLMOCL 371
OY 354 LSPPDSIKM 362
Db 372 LSEGDKVKM 380

RESULT 10
QBEB77
glycoprotein I precursor - human herpesvirus 1 (strain 17)
C:Species: human herpesvirus 1
A:Note: host Hologram #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
Accession: FJMA05243
Release: 1990-07-02Jan, A.; Donald, S.; Rixon, F.J.
K.Motoc Biol 181 1-13, 1985
F:Title: Sequence determination and genetic content of the short unique region in the ge
A:Reference-number: A00656; MWID:85160822; PMID:2984429
A:Accession: A05243
A:Molecule type: DNA
A:Residues: 1-390 <MSG>
A:Cross-references: GB:I00036; NID:g291490; PIDN:AAA96861.1; PID:g291497
C:Genetics:
A:Gene: US7
C:Superfamily: herpesvirus US7 protein
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-390/Product: glycoprotein I #status predicted <GP1>
F:27-293/Domain: transmembrane #status predicted <TM>
F:156,175,257/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 113.5; DB 1; Length 390;
Best Local Similarity 20.8%; Pred. NO. 0.12;
Matches 72; Conservative 63; Mismatches 150; Indels 61; Gaps 15;

OY 7 TALLAATLAFPGAGVITGNHNSARIDDDHIIVAPREATIOLQIFMPGQRPKP- 65
1:::1::: 11:1

Db 27 TVSLANSSEFDVGALE-----PDGVVEADLLS
OY 66 YSGTVAAFRSDITNOCYOELESEERFNCHRSSVFQCCKYTEFTFSARKLTPHPPE 125
Db 70 YDGVEL-WHYPRGHRCPEVVAVVTVACRRRAVAFALCRATDTBS-----PAYPT 121
OY 126 -----KLIRNPNRDNDSGMETVYRIIDDKTEPIDVEAIALSVQEPANTATRELVS 176
Db 122 LEMLAQOPRLRYQRYAGVYLAKVWDPA-N-ASLFVGLMIAMEGLAVNGSAV- 179
OY 177 KASCRIFGLEPTVOLEAYIRLITESHRNQAOAVATGATTSAGENT--PPEVITASELEE 235
Db 160 -GSDPEPLDS-----SARLNPASVVPANQASPTSTTSPSTIPDAVSTIPA--QAS 234
OY 236 HTFTPMLE-----NGVDHEPTPATNENSVTRIGCTMSPLLGGVAAVASTAGLVIV 290
Db 235 TTFFPDDEPKPGPGVNHPFS-----NATRTRDSRFALTIVOIOIALPASIATLVLG 290
OY 291 SIVRNMCTPIHRKLDIVSQDEERSQTRRSKRKGPVACEIKCA 336
Db 291 SCI-----CFTHR-----CQRXRNRSRRTYSPOWPTGISCAVNEA 327

RESULT 11
A61162
glycoprotein I - equine herpesvirus 1 (strain Ab1) (fragment)
C:Species: equine herpesvirus 1
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 23-Aug-1996
Accession: A61162
Release: 1994-09-09Am, J. Vet. Res. 52, 1252-1257, 1991
F:Title: Location of open reading frames coding for equine herpesvirus type-1 glycopr
A:Reference number: A61162; MWID:92027094; PMID:1656822
A:Accession: A61162
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-149 <ELTV>
A:Note: translation of the nucleotide sequence is not complete
C:Superfamily: pseudorabies virus glycoprotein gp63
C:Keywords: glycoprotein
F:27,59,70,113,123/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 6.0%; Score 111.5; DB 2; Length 149;
Best Local Similarity 23.3%; Pred. NO. 0.052;
Matches 35; Conservative 33; Mismatches 69; Indels 13; Gaps 5;

OY 2 ASHLGTLALATLAFPGANGVITGNHNSARIDDDHIIVAPREATIOL-QIFMPGO 60
1:::1::: 11:1
Db 2 AAILISMALCSY-----AIIYRGHSMTLNMSERFAYPDQSLVALGLFLDOO 53
OY 61 R-PHKYSGTVAAFRSDITNOCYOELESEERFNCHRSSSVFGC--KTYEFTFSARK 117
1:::1::: 11:1
Db 54 RLFTTVSLIEL-IHWYSSVCYVLOTISTESCPRANNATFSCIAKTSKHHDYFV 112
OY 118 LTGPHPPEKLIRNPNRDNDSGMETVYRIID 147
1:::1::: 11:1
Db 113 NASVETNVLNITKFPQIDSOAVILKVKLD 142

RESULT 12
C39725
hypothetical protein (Ms11.5' region) - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Feb-1997
Accession: C39725
Release: 1992-02Samuels, B.E., II 3584-3602, 1991
Mol Cell Biol 11 3584-3602, 1991
F:Title: The complex set of late transcripts from the *Drosophila* sex determination ge
A:Reference number: A39725; MWID:91260708; PMID:1710769
A:Accession: C39725
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <SAM>

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GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:06:38 ; Search time 15.5 Seconds
(without alignments)
968,673 Million cell updates/sec

Title: US-09-993-777-7
Sequence: 1 MASLICTLALATLAPFA.....VELVAIVNPSALSPDSIKK 362

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162.5	8.7	354	1 VGLI_VZVD	P09258 varicella-z
2	155	8.3	353	1 VGLI_VZVD	004547 simian vari
3	153.5	8.2	424	1 VGLI_HSVB	P18553 equine herp
4	143.5	7.7	380	1 VGLI_PSVYR	P07646 pseudorab
5	140.5	7.5	380	1 VGLI_HSVB	008102 bovine herp
6	115	6.2	457	1 CD4_MOUSE	P06332 mus musculu
7	113.5	6.1	390	1 VGLI_HSV11	P06487 herpes simp
8	108	5.8	372	1 TUP1_YEAST	P16649 saccharomyc
9	107	5.7	372	1 VGLI_HSV23	P03291 herpes simp
10	99	5.3	372	1 VGLI_HSV2H	P03291 herpes simp
11	99	5.3	1036	1 P200_MTCOPN	P75405 mycoplasma
12	98.5	5.3	1140	1 YD76_MTCOPN	P75405 mycoplasma
13	98	5.3	503	1 CD44_RAT	P26051 ratclut norv
14	98	5.3	507	1 VGLI_YEAST	P33301 saccharomyc
15	97	5.2	1220	1 SLN1_YEAST	P39328 saccharomyc
16	95.5	5.1	797	1 VGLX_HSVB	P28968 equine herp
17	93.5	5.0	907	1 VGLI_MOUSE	P03200 epstein-barr
18	93	4.9	1051	1 NOT3_YEAST	O04127 mus musculu
19	91	4.9	836	1 YS89_CABEL	P06102 saccharomyc
20	91	4.9	3178	1 ICA3_HUMAN	Q09624 caenorhabdi
21	90.5	4.9	547	1 YS89_CABEL	P22942 homo sapien
22	90.5	4.9	785	1 YS89_CABEL	O14758 caenorhabdi
23	90.5	4.9	1429	1 YS89_CABEL	O14758 caenorhabdi
24	88.5	4.8	344	1 ULB6_HCMVNA	P16833 human cytom
25	88	4.7	376	1 POS_FUGRU	P33450 fugu rybkrip
26	86.5	4.6	1037	1 YHIV_ECOLI	P37637 escherichia
27	86	4.6	430	1 YHIV_ECOLI	O07731 mycobacteri
28	86	4.6	636	1 YNR6_YEAST	P53882 saccharomyc
29	85.5	4.6	503	1 PODX_MOUSE	O910M4 mus musculu
30	85	4.6	376	1 MID2_YEAST	P36027 saccharomyc
31	85	4.6	583	1 CH12_CANAL	P40953 candida alb
32	85	4.6	812	1 FGRL_XENLA	P22182 xenopus lae
33	85	4.6	1718	1 RRPO_SHVX	O04575 shallow vir

34	84.5	4.5	440	1 T108_HUMAN	O:4763 homo sapien
35	84.5	4.5	678	1 V1D2_ACRPH	P13463 agrobacteri
36	84.5	4.5	1049	1 ITA3_HUMAN	P08648 homo sapien
37	84.5	4.5	1058	1 ITA3_HUMAN	P22314 homo sapien
38	84.5	4.5	2738	1 PEGV_RAT	O88794 rattus norv
39	84.5	4.5	5376	1 ZAN_MOUSE	O88799 mus musculu
40	84	4.5	536	1 CNAC_RAT	P14644 rattus norv
41	84	4.5	1640	1 CLH2_HUMAN	P53675 homo sapien
42	83.5	4.5	586	1 YEJM_ECOLI	P23922 escherichia
43	83.5	4.5	655	1 CD44_MOUSE	P15370 mus musculu
44	83.5	4.5	881	1 YJH8_YEAST	P17023 saccharomyc
45	83.5	4.5	903	1 BCLC_BOVIN	P34201 bos taurus

ALIGNMENTS

RESULT 1
VGLI_VZVD STANDARD: PRT: 354 AA.
ID VGLI_VZVD
AC P09258:
DT 01-MAR-1989 (Rel. 10, last sequence update)
DT 01-MAR-1989 (Rel. 10, last sequence update)
DT 01-OCT-1996 (Rel. 34, last annotation update)
DE Glycoprotein I precursor (Glycoprotein IV) (GI) (GPV).
GN 67.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OC NCBI_TaxID=10338;
RN (1)
RP SEQUENCE FROM N.A. PubMed=3018124;
RX MEDLINE=86106577; PubMed=6321154;
RA Davidson A.J., Scott J.E.;
RT The complete DNA sequence of varicella-zoster virus *;
RL J. Gen. Virol. 67:1753-1816(1986).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84131932; PubMed=6321154;
RA Davidson A.J.;
RT "DNA sequence of the US component of the varicella-zoster virus genome.";
RN EMBO J. 2:2203-2209(1983).
RT genome.*;
RN [3]
RP MUTAGENESIS, AND PHOSPHORYLATION SITE.
RX Yeo Z., Grosse C.;
RT MEDLINE=94267879; PubMed=8207795;
RN [4]
RP "Unusual phosphorylation sequence in the gpIV (gI) component of the varicella-zoster virus gpI-gpIV glycoprotein complex (VZV gE-gI complex).";
RT J. Virol. 68:4204-4211(1994).
RN [5]
RP J. SUBUNIT: HETERODIMER OF GPV AND GPI (GE).
RN [6]
RP I- SUBCELLULAR LOCATION: Type I membrane protein.
RN [7]
RP I- SIMILARITY: TO HERPESVIRUSES GLYCOPROTEINS I, AND TO PRV GP63.

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EMBL: X04370: CAA7950.1; -;
EMBL: X00208: CAA25032.1; -;
PIR: F27345: VGBB67.
DR InterPro: IPR002874: Herpes_gI.
DR Pfam: PF01688: Herpes_gI; 1.
KW Glycoprotein, 1, 17
KW SIGNAL 354
KW CHAIN 18
KW DOMAIN 18
KW TRANSMEM 296
KW POTENTIAL.
KW POTENTIAL.
KW EXTRACELLULAR (POTENTIAL).
KW POTENTIAL.

```

FT DOMAIN 313 354 CYTOSOL PLASMIC (POTENTIAL).
FT MOD_RES 343 343 PHOSPHORYLATION.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 338 338 T->A: NO EFFECT ON PHOSPHORYLATION.
FT MUTAGEN 341 342 EE->AA: MODERATE DECREASE IN PHOSPHORYLATION.
FT MUTAGEN 343 343 S->A: MARKED DECREASE IN PHOSPHORYLATION.
FT MUTAGEN 344 344 P->A: MARKED DECREASE IN PHOSPHORYLATION.
FT MUTAGEN 345 345 P->A: DECREASE IN PHOSPHORYLATION.
SQ SEQUENCE 354 AA: 39364 MW: 552806 DB08F52E66 CRC64.

Query Match 8.7%; Score 162.5; DB 1; Length 354;
Best Local Similarity 22.4%; Pred. No. 2.6e-06;
Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

QY 23 IVTGNHVSARIDDDHIVAPRPE--ATIQQLFPMGQRP-HKPYSGTVNAERSDI 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
21 LIRKGDHVSILQVNSSLTSLILPMQNDNYTEIKQLVFIQDLPTGTNYSTLELLX-ADT 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 VAFCFRSVOYIRKIDGCPRTTSAPISCRKXSHWHGNSIDRISTEPDAGVMLITPQIN 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 136 DSGMFYVIRALDDTKEPIDVFAIQLSVY-----OFANTATRGYSKAS 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 140 DAGVYVLLVLDHRSR--TQDFILGVNVTYTGSHNHIGVITYTSPSLONGSTALFQQA- 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 CRFFGLPT-----VLEAVLRTEES-WRNMOAVYVATEATTSAEATTPPVPT 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 198 -RCDLPAPPKGSGTSLFOHMLDRAGKSLSDNPWLH-EDVVTETKSVYKEG----- 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 226 ATASELEAEHFTFPMLENCVDHYEPTPAE---ENS-----NVTYRLGTMSPTLIGVY 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 -----IEN---HYFPRDMSLTLEKSLNDPENLLI-----IIPVA 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 277 AAVVSATIGLVISIVTRNM 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 282 SVMILTMVIVIVISVRRRI 302
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
VGLI_SVVD STANDARD: PRT: 353 AA.
ID VGLI_SVVD
AC 004547;
DT 01-JUN-1994 (Rel. 29, Created)
RT 01-JUN-1994 (Rel. 29, Last sequence update)
RL 01-OCT-1996 (Rel. 34, Last annotation update)
GLycoprotein I precursor (Membrane glycoprotein 1).
GI OR 053.
OS Simian varicella virus (strain DHV) (Cercopithecine herpesvirus 9).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
NCBI_Taxid=36348;
OX NCB1_Taxid=36348;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE=9312509; PubMed=8384754;
RT Fletcher T.M. III, Gray W.L.;
RL "DNA sequence and genetic organization of the unique short (US)
region of the simian varicella virus genome.";
Virology 193:762-773(1993).
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GRIV,
AND TO PRV GP63.
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CC or send an email to licenset@sb-sib.ch).
CC EMBL: L07067; AAA47888.1; -
DR PIR: C46113; C46113.
DR InterPro: IPR002874; Herpes_gI.
DR Pfam: PF01668; Herpes_gI.1.
KW Glycoprotein; Transmembrane; Signal.
FT CHAIN 1 20
FT SIGNAL 1 20
FT DOMAIN 21 353
FT TRANSMEM 21 274
FT TRANSMEM 275 293
FT DOMAIN 294 353
FT CARBOHYD 40 40
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 122 122
FT CARBOHYD 138 138
FT CARBOHYD 227 227
FT CARBOHYD 252 252
SQ SEQUENCE 353 AA: 40470 MW: E0314F7B5B0E4AA2 CRC64;

Query Match 8.3%; Score 155; DB 1; Length 353;
Best Local Similarity 20.2%; Pred. No. 1.1e-05;
Matches 65; Conservative 66; Mismatches 151; Indels 40; Gaps 11;

QY 18 FG---AMGITGNHVSARIDDD--HIVAPRPEATIQQLFPMGQRP-HKPYSGTVR 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 20 FGICQAAALIRGNVYISLVNSSATSLFLKGNNDASIRGRFLIGDQPVTVNVTVE 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 VAFRSITNOCYELSEERENCNTHRSSSVFVCGKY-TETTFASNRLTGPPPKLITR 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 L-LHVNOTTLCLOPLRVWGECPRIETGAILICRVKRSWHYVNAQLDNPVEILFKM 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 131 NRPNDGMYVIRALDDTKEPIDVFAIQLSVYOFANTATRGYSKASCTFGJLPTVOL 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 139 NTKVEDAGIYLLVOLDYT-SLEDFIVSLNVPKPDTSMEDVNY-----PPVYS 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 191 EAV-LRTESWRNMOAVYVATEATTSAEATTPPVATSASELEAEHFTFPMLENCVDHY 249
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 PSHILMTFKICHKFPVHNGMEOSILOHIYV-----SDVDTENLSMOKDLGST 238
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 250 EPTPANENSVTVRL-----GTMSPTLIGVYAAVVSATIGLVISIVTRNM 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 239 QKPRKKNPDVKAVNVTHERKKTLMESADVEMTAVPTASLVILAITIIVTGIRRS 298
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 299 TPHRKLDIVSQDDERSQTRRE 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 299 SEKRKIYRPRKTEQASTEKRE 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
VGLI_HSVB STANDARD: PRT: 424 AA.
ID VGLI_HSVB
AC P18553;
DT 01-NOV-1990 (Rel. 16, Created)
RT 01-NOV-1990 (Rel. 16, Last sequence update)
RL 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glycoprotein I precursor.
GI OR 73.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and
OS Equine herpesvirus type 1 (strain ABI) (EHV-1), and
OS Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
NCBI_Taxid=31520; 10328, 10330;
OX NCB1_Taxid=31520; 10328, 10330;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=AB4p;
RX MEDLINE=92295566; PubMed=1318606;
RT Tedford E.A.R., Watson M.S., McBride K., Davison A.J.;
RL "The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316(1992).
[2]

```

RP SEQUENCE FROM N.A.
 RC STRAIN-AB1;
 RA MEDLINE-91276272; PubMed-1647359;
 RA Elton D.M., Halliburton I.W., Killington R.A., Meredith D.M.,
 RA Bonass W.A.;
 RT "Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine
 RT herpesvirus type-1 short unique region."
 RT Gene 101:203-208(1991).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-Kentucky D.
 RC MEDLINE-9108333; PubMed-2177089;
 RA Audonnet J.C., Henslow J., Allen G., Paolletti E.;
 RA Equine herpesvirus type 1 unique short fragment encodes
 RT glycoproteins with homology to herpes simplex virus type 1 gp, g1 and
 RT g2.
 RT J. Gen. Virol. 71:2969-2978(1990).
 RL J. Gen. Virol. 71:2969-2978(1990).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
 CC AND TO PRV GP63.
 CC -----
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 CC -----
 DR EMBL: M86664; AAB02508.1;
 DR EMBL: M36646; VGBHE9.
 DR PIR: C36646; VGBHE9.
 DR PIR: J00998; J00998.
 DR PIR: A36803; VGBEG4.
 DR InterPro: IPR002874; Herpes-g1.
 DR Pfam: PF01688; Herpes-g1.1.
 DR Glycoprotein: Signal; Transmembrane.
 KM SIGNAL: 1 22
 FT CHAIN: 23 424
 FT DOMAIN: 23 319
 FT TRANSMEM: 320 340
 FT DOMAIN: 341 424
 FT CARBOHYD: 35 35
 FT CARBOHYD: 67 67
 FT CARBOHYD: 78 78
 FT CARBOHYD: 121 121
 FT CARBOHYD: 131 131
 FT CARBOHYD: 236 236
 FT CARBOHYD: 307 307
 SEQUENCE 424 AA; 46392 MW; E9BEF7DA895806 CRC64;
 Query Match 8.28; Score 153.5; DB 1; Length 424;
 Best Local Similarity 23.88; Pred. No. 1; 9e-05;
 Matches 70; Conservative 41; Mismatches 126; Indels 57; Gaps 12;
 OY 1 MASLLGTALLAATLAPFGAMGIVTGNHVSARIDDDHIVYAPREBATIOL-QLPFMG 59
 DB 1 MAKLTGMSAAILLSMAICSAIILYRGHSMMLNSSFAYLFDOSLVVGHLEFDIG 60
 OY 60 QR-PHKRYSGTVAFRSDITNOCYOELSEREFENCNTHRSSVFVGC--KYTEYTSASN 116
 DB 61 ORLPPTNYGLIEL-IHNYMSVCTVYQIYTESCPRYANNAFSCCHKTSKHYADYR 119
 OY 117 RUTGPRHPFKLTIRNRPNDSGMFYIVRLDQTKEDIDVFAIOLSVYQFANTATRG 176
 DB 120 VNASVETNVLINIKKQPDPSGAYILRKIDHA-PTADVFQVSAVYDL----- 167
 OY 177 KASCRFTGLPTVO---LEAYLRTEESMRMNOAVVATEATTS---AAATPTPTVATSA 229
 DB 168 KSKIVPDMPTTQTVPEPTTSYVSTPTDYDTDEETESTISTOOAMTSTQTP-SATWG 226
 OY 230 SELEAHEHTPMLNGVDHDEPTPANENSNTYVLG-----TMSPTL 271

DB 227 TQLTLE-----LPTNE-----TVVIGQALLCHWQDPSTREPTL 260
 RESULT 4
 ID VGLI_PVRI STANDARD: PRT; 350 AA.
 AC P0746;
 DT 01-APR-1988 (rel. 07, Created)
 DT 01-APR-1988 (rel. 07, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Glycoprotein GP63 precursor.
 OS Pseudorabies virus (strain Rice) (PRV).
 OC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicelloviruses.
 NC NCBI TaxID=10350;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA MEDLINE-86308235; PubMed-3010284;
 RA Petrovskis E.A., Timmins J.G., Post L.E.;
 RA "Use of lambda g11 to isolate genes for two pseudorabies virus
 RT glycoproteins with homology to herpes simplex virus and varicella-
 RT zoster virus glycoproteins."
 RT J. Virol. 60:185-193(1986).
 RL J. Virol. 60:185-193(1986).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, AND TO VZV
 CC GP1V.
 CC -----
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 CC -----
 DR EMBL: M14336; AAC35204.1;
 DR PIR: A29012; VGBE63.
 DR InterPro: IPR002874; Herpes-g1.
 DR Pfam: PF01688; Herpes-g1.1.
 DR Glycoprotein: Transmembrane; Signal.
 KM SIGNAL: 1 23
 FT CHAIN: 24 350
 FT DOMAIN: 24 285
 FT TRANSMEM: 286 308
 FT DOMAIN: 309 350
 FT CARBOHYD: 56 56
 FT CARBOHYD: 73 73
 FT CARBOHYD: 153 153
 FT CARBOHYD: 256 256
 FT CARBOHYD: 262 262
 FT CARBOHYD: 275 275
 SEQUENCE 350 AA; 36773 MW; 66AF229EC21BEDA CRC64;
 Query Match 7.78; Score 143.5; DB 1; Length 350;
 Best Local Similarity 22.88; Pred. No. 0.0001;
 Matches 82; Conservative 42; Mismatches 149; Indels 87; Gaps 17;
 OY 8 LALLAATLAPFGAM--GIVTGNHVSARIDDDHIVYAPREBATIOL-QLPFMG 65
 DB 15 LLLAALLAALLAPRGVGLFPGAGSVHVGASVAVLPGDAPVLVLDGTLFLFGPSPS- 73
 OY 66 YSGTVAFRSDITNOCYOELSEREFENCNTHRSSVFVGC--KYTEYTSASN 118
 DB 74 YSGFVEL-LRLDPRKACRYTREAEDYLCRVVHNEFRCCCKRKPRLARRASAAVAPRL 132
 OY 119 TGPHPHPFKLTIRNRPNDSGMFYIVRLDQTKEDIDVFAIOLSVYQFANTATRG 174
 DB 123 -----LFSRNPAPDAGSVYLRVNGT---TDLFLVLAIV-----PRGPRHP 174
 OY 175 -YSKASCRFTGLPTVOLEAVLRTEESMRMNOAVVATEATTS---AAATPTPTV 224
 DB 175 TPSSADCR-----PV-----GSMHSLRVDPADAVFTTPPIEPEPTTPAP 221

OY 225 TATSAS-----ELEAEHFTPEWLENGVDHYEPANENSNTVRLGWSPTLIGVTA 277
 DB 222 RGTGATPEPSDEDEDEDE-----EGATATAMPVPGTDLANGT-----VLNASVSVLL 271
 OY 278 AVVSATG-----LVIVISIVTRMNCIPHRKLDIVSODDERSGOTRRRSRK 323
 DB 272 AANAATGANGAPCKIAMVGLPTIVLILFVGAVCAARRCARGIASTGRCAGARRSTR 331

RESULT 5
 VGLI_HSVBS STANDARD: PRT: 380 AA.

AC 008102;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Glycoprotein I.
 GN GI.
 OS Bovine herpesvirus type 1.2 (strain ST).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 NC Alphaherpesvirinae; Varicelloviruses.
 NCBI_Taxid=45407;

RP SEQUENCE FROM N.A.
 RX MEDLINE-94167875; PubMed-8122370;
 RA Leung-Trick P., Audonnet J.F., Riviere M.;
 RT "The complete DNA sequence and the genetic organization of the short
 unique region (US) of the bovine herpesvirus type 1 (ST strain).";
 RL Virology 199:409-421(1994).
 CC -1- SIMILARITY: NO OTHER HERPESVIRUSES GLYCOPROTEIN I, TO VZV GIV,
 AND TO PRV GP63.

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 CC -----

DR EMBL: 223068; CA80605.1;
 DR InterPro: IPR002874; Herpes_gi.
 DR Pfam: PF01688; Herpes_gi.1.
 KW Glycoprotein.

FT CARBOHYD 67
 FT SEQUENCE 380 AA: 39910 MM: AEBELFB9B430D2BD CRC64: (POTENTIAL).

Query Match 7.5%; Score 140.5; DB 1: Length 380;
 Best local similarity 25.3%; Pred. No. 0.0002;
 Matches 68; Conservative 33; Mismatches 125; Indels 43; Gaps 9;

OY 1 MASLLTLLAATLAPFGAMGIVITGNHVSARIDDIIVAPREPATIQ--OLEFMP.58
 DB 1 MRCLLLMVYLARAP--ARSLYRGEAVGLRAGPVAFVHP--TDATLALGRILFLE 57
 OY 59 GQRP-HKPSVSGTVARVAFRSITNOCYOELSEEFENCSTHRSSEVPFGCKVETTFASNR 117
 DB 58 HQPAGRRNGVEL-LRYHAAGDCVMTQTFAFCSPRYANNAFNSCLHADRPARSER 116
 OY 118 LTGP--PHPEFKLTIRNPDPDSGMFYIVRL---DDTKEDIVPAIQLSVYQFA----- 166
 DB 117 RASAVENHVFLEFIARPRIDSLYFLRNGITYGCTAGSENRROVFFLAAPHVHGFEGBDP 176
 OY 167 -----NTAATRGILYSKASCRTEGL-----PTVQLEAVYLRTEESWR 201
 DB 177 EAAARTPARSGRSPASGITSASLYDRALANSPQAPPRAAPRAAARGPRRPERVDE 236
 OY 202 NMOAVATEATTTSACATITPTPTATAS 230
 DB 237 TTEVAATRASAFALTTPAGTASPA 265

RESULT 6

CD4_MOUSE
 ID CD4_MOUSE STANDARD: PRT: 457 AA.
 AC P06332;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
 T4/Leu-3) (T-cell differentiation antigen L3T4).
 GN CD4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87018845; PubMed-3094146;
 RA Tourville B., Gorman S.D., Field E.H., Hunkapiller T., Parnes J.R.;
 RT "Isolation and sequence of L3T4 complementary DNA clones: expression
 in T cells and brain."
 RL Science 234:610-614(1986).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87115821; PubMed-3027575;
 RA Littman D.R., Gettner S.N.;
 RT "Unusual Intron in the Immunoglobulin domain of the newly isolated
 murine CD4 (L3T4) gene."
 RL Nature 325:453-455(1987).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX TISSUE-brain;
 RX MEDLINE-88152875; PubMed-3326818;
 RA Parnes J.R., Hunkapiller T.;
 RT "L3T4 and the immunoglobulin gene superfamily: new relationships
 between the immune system and the nervous system."
 RL Immunol. Rev. 100:109-127(1987).
 RN (4)
 RP SEQUENCE FROM N.A. (BRAIN FORM).
 RC TISSUE-brain;
 RX MEDLINE-88041359; PubMed-2823269;
 RA Gorman S.D., Tourville B., Parnes J.R.;
 RT "Structure of the mouse gene encoding CD4 and an unusual transcript
 in brain."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).
 RN (5)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98112780; PubMed-9445485;
 RA Ansari-Pari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
 Gibbs R.A.;
 RT "Comparative sequence analysis of a gene-rich cluster at human
 chromosome 12p13 and its syntenic region in mouse chromosome 6."
 RL Genome Res. 8:29-40(1998).
 RN (6)
 RP SEQUENCE OF 27-43.
 RX MEDLINE-86166694; PubMed-3082751;
 RA Classon B.J., Tsagaratos J., Kirszenbaum L., Maddox J., McKay C.R.,
 Braden M., McKenzie I.F.C., Walker I.D.;
 RT "The L3T4 antigen in mouse and the sheep equivalent are
 immunoglobulin-like."
 RL Immunogenetics 23:129-132(1986).
 RN (7)
 RP DISULFIDE BONDS.
 RX MEDLINE-86233454; PubMed-3086886;
 RA Classon B.J., Tsagaratos J., McKenzie I.F.C., Walker I.D.;
 RT "Partial primary structure of the T4 antigens of mouse and sheep:
 assignment of intrachain disulfide bonds."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
 CC -1- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
 CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
 CC -1- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC
CC EMBL: M36850: AAA39401.1;
CC EMBL: M13816: AAA37267.1;
CC EMBL: X04836: CAA28539.1;
CC EMBL: M36851: AAA39402.1;
CC EMBL: M17080: AAA37403.1;
CC EMBL: M17078: AAA37403.1; JOINED.
CC EMBL: M17079: AAA37403.1; JOINED.
CC EMBL: AC002397: AAC36010.1;
CC PIR: A02110: RMMST4.
CC PIR: A26038: A26038.
CC HSSP: P01730: 1WBR.
CC MGD: MGI:88335: Ccd4.
CC InterPro: IPR000973: CD4_TCAg.
CC InterPro: IPR003006: Ig_MHC.
CC InterPro: IPR003600: Ig_Like.
CC InterPro: IPR003596: Ig_V.
CC Pfam: PF00047: Ig_1.
CC PRINTS: PR00692: CD4TCANTIGEN.
CC SMART: SM00410: Ig_Like; 2.
CC SMART: SM00406: IgV_1.
CC Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
CC Immune response; Repeat; Signal; Lipoprotein; Palmitate;
CC Alternative splicing.
CC FT CHAIN 1 26
CC FT DOMAIN 27 457
CC FT TRANSSEM 395 417
CC FT DOMAIN 418 457
CC FT DOMAIN 418 457
CC FT DOMAIN 129 207
CC FT DOMAIN 208 317
CC FT DOMAIN 318 374
CC FT CARBOHYD 187 374
CC FT CARBOHYD 296 325
CC FT CARBOHYD 325 353
CC FT CARBOHYD 352 392
CC FT DISULFID 152 188
CC FT DISULFID 328 370
CC FT DISULFID 418 421
CC FT LIPID 421
CC FT UNUSUAL 1 240
CC FT SEQUENCE 457 AA: 51296 MW: 181DA7527CB00F33 CRC64;
CC
CC Query Match 6.2%; Score 115; DB 1; Length 457;
CC Best Local Similarity 20.6%; Pred. No. 0.035;
CC Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;
CC
CC 19 GAMGIVITGNHVSARIIDDDHIVAPREATTIOLTF--FMFGQRPKPYSGTVRAFR 75
CC 93 GSFPLIT--NLIKMDSQTYICELNREK--EVELWVFKYFSGTSLGQSLTLLTDSN 149
CC 76 SDITNOCYOELSEERFENCNTHSSSVFQCKVETFTYPSANRLTGPFPFKUTLRPN 135
CC 150 SKVSN---PLTE---CKHKRGVYVSGSKV-----LSMSNRVQ 181
CC
CC 136 DSGMYVIVRLDITKEPIDVFAIQSVYOFANTATAGLYSKASCRTQLPLVQLEAYLR 195
CC 182 DSDFNCTVTLDOKK--NMFGWTLVGLFQSTAIT--AVYSBESAESFPLNARE----- 233
CC 196 TEBSNRN--WQAVYVTEATTSSAETPTPTVATASASELAEHFTPEPLNCOVHYETP 253
CC 234 -ENMGELMKWA-----KDSFQPMISFINKKEYSV 265

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CC 254 ANENSVTVRLGTSMTPLIGVAVAVSATIGLIVITVTRNCKTPHRLTYSODDEE 313
CC 266 QKSTNKLQKLKELPLPLKIPVSLQFAGSGLN---TLTLDKGLHOENVLYMKVAQ 321
CC 314 RSCTRESKPKPMVACEIN-----KGAQD---SELVELVAIVNPSA----- 353
CC 322 LNT-----LTCEVMGPTSPKMLTLKQENQEARVSEOKVQVAVAPETGLMOCL 371
CC 354 LSSPDSIKM 362
CC 372 LSEGDYKM 380
CC
CC RESULT 7
CC ID VGLI_HSV11 STANDARD: PRT; 390 AA.
CC AC P06487;
CC DT 01-JAN-1988 (Rel. 06, Created)
CC DT 01-JAN-1988 (Rel. 06, Last sequence update)
CC DT 01-OCT-1996 (Rel. 34, Last annotation update)
CC DE Glycoprotein I.
CC GI OR US7.
CC OS Herpes simplex virus (type 1 / strain 17).
CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC NCBI_TaxID=10299;
CC RX MEDLINE=85160822; PubMed=2984429;
CC RA McGeeoch D.J., Dolan A., Donald S., Rixon F.J.;
CC "Sequence determination and genetic content of the short unique
CC region in the genome of herpes simplex virus type 1."
CC J. Mol. Biol. 181:1-13(1985).
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GE, AND GF.
CC -1- SIMILARITY: TO OTHER HERPESVIRUS GLYCOPROTEINS I, TO VZV GIV,
CC AND TO PRV GP63.
CC
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CC
CC EMBL: L00036: AAA06681.1;
CC EMBL: X41118: CAA32284.1;
CC EMBL: X02438: CAA26061.1;
CC PIR: A05243: OCBE77; Herpes_GI.
CC InterPro: IPR002874: Herpes_GI.
CC PIR: P01688: Herpes_GI_1.
CC Glycoprotein I.
CC CARBOHYD 156 156
CC CARBOHYD 175 175
CC CARBOHYD 257 257
CC FT SEQUENCE 390 AA: 41369 MW: 3938181D65F0808 CRC64;
CC
CC Query Match 6.1%; Score 113.5; DB 1; Length 390;
CC Best Local Similarity 20.8%; Pred. No. 0.038;
CC Matches 72; Conservative 63; Mismatches 150; Indels 61; Gaps 15;
CC
CC 7 TLTLAATLAPFGAMGIVITGNHVSARIIDDDHIVAPREATTIOLTFMFGQRPK 65
CC 27 TVSLVSNSEFVADALG-----PDGVVBEEDLLTD-----EURFVGQVPHITV 69
CC
CC 66 YSGTVRAVAFSDITNOCYOELSEERFENCNTHSSSVFQCKVETFTYPSANRLTGPFP 125
CC 70 YDGVGL-WHYPRGHCRCPRVHVYVATACRRPAVAFALCRATIDSHS-----PAYET 121
CC 126 -----KLTIRNRPNDSGMYVIVRLDITKEPIDVFAIQSVYOFANTATAGLYS 176

```


OS Herpes simplex virus (type 2 / strain 333).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10313;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86291145; PubMed=3016980;
RA Hodgman T.C., Minson A.C.;
RT "The herpes simplex virus type 2 equivalent of the herpes simplex
virus type 1 US7 gene and its flanking sequences."
RT Virology 153:1-11(1986).
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEIN IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
CC AND TO PRV GP63.
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CC
CC EMBL: M14886; AAA45861.1; -
CC EMBL: D00026; BA00021.1; -
CC PIR: A05246; Q08888;
CC InterPro: IPR002874; Herpes_g1.
CC Pfam: PF01688; Herpes_g1; 1.
CC
CC Glycoprotein.
KW CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 AA: 39548 MW: BB3A9E2D20B8ADBD CRC64;
SQ
Query Match 5.78; Score 107; DB 1; Length 372;
Best Local Similarity 21.08; Pred. No. 0.12; 163; Indels 64; Gaps 13;
Matches 74; Conservative 51; Mismatches 163;
OY 3 SLGTTALLAATLAFGAMGIVITGNVNSARIDDDHIVAPREAIOL-----QLFF 56
DB 5 SLOG-LAILGLWVC---ATGLVNGPTVSL-VSDSLVDAGANGPGVEEDLAVFGELHF 59
OY 57 MGGORPKPKSGTVAVARSDITNOQOESEERFENCNHRSSVFGCKVTEYTSASN 116
DB 60 VGAOVPHNTNYDGIIELEHPLGNHCRVHVHTLACRRRAVAFTLCRSTHANS--- 116
OY 117 RUTGPRHPF-----KLITRNPNDGSMFYVIRLDD-TKEPIDVFIOLSYOFA 166
DB 117 ---PAPFLELGLAROPILNRATRDYAGLYLVHVGASATNSLFLGVALS---A 168
OY 167 NTAATRGIVSKASCRFTGLPTVOLEAVLRTEESRMWQVYVATEITTSAGATPPPTA 226
DB 169 NGTFVNGSYGSCDPAQLP-----FSAPRLGSPSYVTPGASPPPPPT 212
OY 227 TSASELEAEHFTPEMLENGVDHYEPTPANENSNVYRLGTMSPTLIGTVAAVVSATIGL 286
DB 213 TTSPSSPRDPTPAFG-----DTGTPAPASGEIAPVNSTSASESHRRLTVAOYIOAIPA 267
OY 287 VIVISIVTRN-MCTPHRKLDIVSODDERSGOTRESKRGKGP-MVACEINKGA 336
DB 268 SLIAFVFLGSCICFIHRC-----QRRYRRPRGCIYNPGVSCAVNENA 310
RESULT 10
VGLI_HSV2H STANDARD: PRT: 372 AA.
AC P13291;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glycoprotein I.

GN GI OR US7.
OS Herpes simplex virus (type 2 / strain HG52).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10313;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=87111457; PubMed=3027242;
RA McGeoch D.J., Moss H.W.M., McNab D., Frame M.C.;
RT "The unique long (UL) gene and genetic content of the HindIII 1 region in the
RT DNA sequence component of the herpes simplex virus type 2 genome:
RT identification of the gene encoding glycoprotein G, and evolutionary
RT comparisons.";
RT J. Gen. Virol. 68:19-38(1987).
CC
CC [2]
CC SEQUENCE FROM N.A.
CC
CC RA Dolan A.;
CC Submitted (FEB-1997) to the EMBL/Genbank/DDAJ databases.
CC -1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEINS I, TO VZV GP1V,
CC AND TO PRV GP63.
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CC
CC EMBL: X04798; CA28485.1; -
CC EMBL: 286099; CAB06714.1; -
CC PIR: F43674; F43674.
CC InterPro: IPR002874; Herpes_g1.
CC Pfam: PF01688; Herpes_g1; 1.
CC
CC Glycoprotein.
KW CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 AA: 39558 MW: C0D4A22CAB16B8D CRC64;
SQ
Query Match 5.38; Score 99; DB 1; Length 372;
Best Local Similarity 21.08; Pred. No. 0.38; 165; Indels 64; Gaps 13;
Matches 74; Conservative 49; Mismatches 165;
OY 3 SLGTTALLAATLAFGAMGIVITGNVNSARIDDDHIVAPREAIOL-----QLFF 56
DB 5 SLOG-LAILGLWVC---ATGLVNGPTVSL-VSDSLVDAGANGPGVEEDLAVFGELHF 59
OY 57 MGGORPKPKSGTVAVARSDITNOQOESEERFENCNHRSSVFGCKVTEYTSASN 116
DB 60 VGAOVPHNTNYDGIIELEHPLGNHCRVHVHTLACRRRAVAFTLCRSTHANS--- 116
OY 117 RUTGPRHPF-----KLITRNPNDGSMFYVIRLDD-TKEPIDVFIOLSYOFA 166
DB 117 ---PAPFLELGLAROPILNRATRDYAGLYLVHVGASATNSRVLGVALS---A 168
OY 167 NTAATRGIVSKASCRFTGLPTVOLEAVLRTEESRMWQVYVATEITTSAGATPPPTA 226
DB 169 NGTFVNGSYGSCDPAQLP-----FSAPRLGSPSYVTPGASPPPPPT 212
OY 227 TSASELEAEHFTPEMLENGVDHYEPTPANENSNVYRLGTMSPTLIGTVAAVVSATIGL 286
DB 213 TTSPSSPRDPTPAFG-----DTGTPAPASGEIAPVNSTSASESHRRLTVAOYIOAIPA 267
OY 287 VIVISIVTRN-MCTPHRKLDIVSODDERSGOTRESKRGKGP-MVACEINKGA 336
DB 268 SLIAFVFLGSCICFIHRC-----QRRYRRPRGCIYNPGVSCAVNENA 310
RESULT 11

P200_MYCPN STANDARD: PRT: 1036 AA.

AC P75211; Q50346;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein P200.
 GN P200 OR MPN567 OR MP275.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE=96257197; PubMed=8675035;
 RA Profit T., Hilbert H., Plagens H., Herrmann R.;
 RT "The P200 protein of Mycoplasma pneumoniae shows common features with
 the cytochrome-associated proteins HmM1 and HmM3.";
 RL Gene 171:79-82(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 RN [3]
 RP SEQUENCE OF 641-678 FROM N.A.
 RC STRAIN-ATCC 29342 / M129; PubMed=7984111;
 RX MEDLINE=95075318; PubMed=7984111;
 RA Profit T., Herrmann R.;
 RT "Identification and characterization of hitherto unknown Mycoplasma
 pneumoniae proteins.";
 RL Mol. Microbiol. 13:337-348(1994).
 CC -1- FUNCTION: PROTEIN CYTOSKELETON-ASSOCIATED WHICH COULD BE AN
 ACCESSORY STRUCTURAL COMPONENT IN CYTADHERENCE.
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 or send an email to license@isb-sib.ch).
 CC EMBL: U25989; AAC99815.1; -
 CC EMBL: AE000027; AAB95923.1; -
 CC EMBL: Z52646; CA63569.1; -
 CC Cytochrome; Structural protein; Repeat; Complete proteome.
 FT DOMAIN 277 280 POLY-THR.
 FT DOMAIN 300 845 PRO-RICH.
 FT DOMAIN 357 360 POLY-THR.
 FT DOMAIN 401 404 POLY-ALA.
 FT DOMAIN 718 781 3 X 6 AA REPEAT OF E-P-E-P-N-F.
 FT REPEAT 718 723 1.
 FT REPEAT 738 743 2.
 FT REPEAT 776 781 3.
 FT CONFLICT 641 641 A -> P (IN REF. 3).
 SQ SEQUENCE 1036 AA; 116915 MW; DESAEBAB6DD95B29 CRC64;

Query Match 5.3%; Score 99; DB 1; Length 1036;
 Best Local Similarity 23.9%; Pred. No. 2.2;
 Matches 57; Conservative 29; Mismatches 90; Indels 62; Gaps 10;

OY 127 LTRNRPRDSCMFYIVRLDTPKEPIDVFAQLSYQFAN--TATRGVLSKASCRFP 183
 DB 446 VVIDNQPPOAGFHYVDFLTST-APLTYAELELOBOELVNEFVTTSTRRTTFFASTPVF 504
 OY 184 G--LPTVLEAVLTREESRMNOAVVATEATTSAEATP--TPVATSASELEAH 236
 DB 505 EPVIVTFVSEBOLLENE-----FVESTIVSATSNPEPNASTPVEVET----- 546

YD76_MYCPN STANDARD: PRT: 1140 AA.

AC P75405;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MPN376 (A19_071140).
 GN MPN376 OR MP460.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
 MPN375.
 CC -2- SIMILARITY: IN THE CENTRAL SECTION; STRONG, TO M.PNEUMONIAE
 MPN374.
 CC -3- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO M.PNEUMONIAE
 MPN373.
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 CC EMBL: AE000045; AAB96108.1; -
 CC Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 8 28 POTENTIAL.
 FT TRANSMEM 1098 1118 POTENTIAL.
 SQ SEQUENCE 1140 AA; 130383 MW; 8FA9406C57DD886 CRC64;

Query Match 5.3%; Score 98.5; DB 1; Length 1140;
 Best Local Similarity 20.5%; Pred. No. 2.7; Mismatches 119; Indels 91; Gaps 15;
 Matches 68; Conservative 53;

OY 71 RFAFRSDITNOC-YQELSERE-NCTHRSSSVFVCKTXYTFSSNRLTGPPHFKLT 128
 DB 680 RERFQKDINNYLKVQGISERIKVNAVHVDAIMLRKSSDPLAS--VQSTANKYGLN 736
 OY 129 IR-NRPNDSCMFYIV--RLLDTK-----EPIDVFAQLSYQFAN-- 167
 DB 737 LRSNPY--TGQFYVVDVDTNANDLGNORANNAKSYFYIIGLDKGAQSSYLVRPENO 793
 OY 168 -----TAAPRGVLSKASCRFGLPTVQLAEVLTREES-----WRMNOAVVATEATT 213
 DB 794 KLYSESLAVDSRGVYK-----NWSKDIIDAKONULYDTHMNA--ALKALU 842
 OY 214 TSAEATTPPVATSASELEAHFPPVLENGVDHYEPPANENSNTVRLGTMSPFLIG 273
 DB 843 TNAELULPT-ASADNSAKIS-----TPNNEDE-----GFLSNVSG 878
 OY 274 VYVAAVVSAFTGLVIVISIVTRNM-----CTPHRKLDTVSODDEBSOTRRE 320

Db 879 SILGYERMTGKFLFKERVSFNKEDNNIKLNTSNTFLDKKLEKVDSEVINOIVEE 938
 Oy 321 SRKFGPMACEINKGADODELVELVAIYVP 351
 Db 939 AKGYNAVSEKGDDESDKNFKITLTNP 969

RESULT 13
 CD44_RAT STANDARD: PRT: 503 AA.
 AC P26051: 099021: (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 41, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CD44 antigen precursor (Phagocytic glycoprotein I) (Pgp-1) (HUTCH-1)
 DE (Extracellular matrix receptor-III) (ECMR-III) (Gp90 lymphocyte
 DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor)
 DE (LY-24).
 CD44.
 NC Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN-BDIX; TISSUE-Pancreas;
 RX MEDLINE-91191552; PubMed-1707342;
 RA Guenther U., Hofmann M., Rudy W., Reber S., Zoeller M.,
 RA Hausmann I., Matzku S., Wenzel A., Ponta H., Herlich P.;
 RT "A new variant of glycoprotein CD44 confers metastatic potential to
 RT rat carcinoma cells.";
 RL Cell 65:13-24(1991).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORMS 1).
 RA Stevens J.W., Midura R.J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAIN CELL SURFACE RECEPTOR FOR HYALURONATE. ADHESION TO
 CC MUCOSAL HIGH ENDOTHELIAL VENULE AND TO TYPES I AND VI COLLAGEN.
 CC PROBABLY INVOLVED IN MATRIX ADHESION, LYMPHOCYTE ACTIVATION AND
 CC LYMPH NODE HOMING.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1/short form and 2/long
 CC form/meta-1 (shown here); are produced by alternative splicing.
 CC -1- PTM: EXTENSIVELY MODIFIED INCLUDING N- AND O-LINKED GLYCOSYLATION.
 CC ADDITION OF THE GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, OR SULFATE,
 CC OF PHOSPHATE TO CYTOPLASMIC DOMAIN SERINE RESIDUES.
 CC -1- SIMILARITY: CONTAINS 1 LINK DOMAIN.

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 EMBL: M61875; AAAS3332.1; -
 DR EMBL: M61874; AAAS3334.1; -
 DR EMBL: U52179; AAAG9151.1; -
 DR EMBL: U46957; AAAG92920.1; -
 DR HSSP: P98066; ITSG.
 DR InterPro: IPR001231; CD44_antigen.
 DR InterPro: IPR000538; Link.
 DR Pfam: PF00193; Xlink; 1.
 DR PRINTS: PR00658; CD44.
 DR PRODOM: PD000918; Link; 1.
 DR SMART: SM00445; Link; 1.
 DR PROSITE: PS01241; Link; 1.
 DR Cell adhesion; Transmembrane; glycoprotein; Phosphorylation;
 KW Receptor; Proteoglycan; Sulfate; Signal; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 503 CD44 ANTIGEN.

FT DOMAIN 22 410
 FT TRANSMEM 411 431
 FT DOMAIN 432 503
 FT DOMAIN 51 123
 FT MOD_RES 56 122
 FT DISULFID 56 122
 FT DISULFID 80 100
 FT CARBOHYD 28 100
 FT CARBOHYD 60 60
 FT CARBOHYD 103 103
 FT CARBOHYD 124 114
 FT CARBOHYD 124 124
 FT CARBOHYD 266 266
 FT CARBOHYD 274 274
 FT CARBOHYD 306 306
 FT VARSPLIC 224 385

FT CONFLICT 74 74
 FT SEQUENCE 503 AA; 55945 MM; FB489D009BDAER22 CRC64.
 FT SQ

Query Match
 Best Local Similarity 22.2%; Pred. No. 1;
 Matches 47; Conservative 30; Mismatches 79; Indels 56; Gaps 10;

Oy 178 ASGRFGPLPTVQLAEVLTREESW--RNNO-----AYVATEATTSAETTPPVY 225
 Db 297 ATSTWADPNSTTEATQKEKFEWNOGNRPPTSDSHV--TEGTTASAHNNHPSORM 355
 Oy 226 ATASELAEHFTPEMLNENGVDHYEP-----TPANSENATVRLGTSP 269
 Db 356 TTSQSE-----DVSW-----TDFEFDISHPMQGHQTESKSHSGSGNDGVTITGSPARR 405
 Oy 270 TLIG---YVAVAVSATIGLVIVTSVTRNMCTPRKLDVTSODDERSGTRESRRKFP 326
 Db 406 PQPEMLITLILSLALILAVCIAVNSRRRCGQKKL--VINSNGTVEDRRPS----- 458
 Oy 327 MVACEINKGADODELVELVAIYVPALSSPD 358
 Db 459 ----ELNGSAKSGQEMVHL--VNKEPTETPD 483

RESULT 14
 YG46_YEAST STANDARD: PRT: 507 AA.
 ID YG46_YEAST
 AC P53301;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 52.8 kDa protein in BUB1-H1P1 intergenic region.
 GN YG189C OR G7953.
 OS Saccharomyces cerevisiae (Baker's yeast)
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OC NCBI_TaxID=4932;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C;
 RX MEDLINE-97279311; PubMed-9133739;
 RA Arroyo J., Garcia-Gonzalez M., Garcia-Saez M.I., Sanchez-Perez M.,
 RA Nombela C.;
 FT "DNA sequence analysis of a 23,002 bp DNA fragment of the right arm
 FT of Saccharomyces cerevisiae chromosome VII.";
 RL Yeast 13:357-363(1997).
 CC -1- SIMILARITY: SOME. TO YEAST UTR2.

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DR EMBL: 272974; CAA97215.1; -
 DR EMBL: X99074; CAA67525.1; -
 DR HSP: P23904; IAKK.
 DR SGD: S0003421; CRH1.
 DR InterPro: IPR00757; Glyco_hydro.16.
 DR Pfam: PF00722; Glyco_hydro.16; 1.
 KW Hypothetical protein.
 FT DOMAIN 63 66 POLY-SER.
 FT DOMAIN 301 310 POLY-SER.
 FT DOMAIN 345 357 POLY-SER.
 FT DOMAIN 387 391 POLY-SER.
 FT DOMAIN 467 470 POLY-SER.
 SO SEQUENCE 507 AA; 52757 MW; 707B61F57AE942C CRC64;

Query Match 5.3%; Score 98; DB 1; Length 507;
 Best Local Similarity 21.7%; Pred.No. 1.1;
 Matches 54; Conservative 46; Mismatches 95; Indels 54; Gaps 9;

136 DSGMFVIRLDPTKPIPIVFAIQLSVQFANTATRGYSKASCRFGLPVQLEAYLR 195
 278 DGSSTI--GRYDQAGDFAVLANGSISSSTSVSSASTSVSSASTSVSSAST 335
 196 TEBSWNRNOAYVATEATTSAEATPTPTVATASASELEAHFTPELVNGVDHYEPTPAN 255
 336 VSSS--VSTVSSSSSSSSSSSTSPSSSTATSSKTLASSVT--TSSSIISFE-KOSS 388
 256 ENSNVTRIGTMTPTLIGT-VAAYVSATLGLIVISYTRNNCTPHRKIDITYSOP---- 310
 389 SSSKRTVASSSTSESTISSTKTPATVSS--TRSTVAPTTQSSVSSDSPVQ 438
 311 -----DEERSQTRRESRKFGPMV-----ACEINKGADOD-----S 340
 439 DKGAVATSSNDVTSSTQTSSKRTSTIQSSSSASSSTNSVQISNGADLQSLPREKITS 498
 341 ELVELVAIV 349
 499 VLVALALL 507

RESULT 15
 ID SLN1_YEAST STANDARD; PRT: 1220 AA.
 AC P39928;
 DT 01-FEB-1995 (Rel. 31, Created)
 RT 01-FEB-1995 (Rel. 31, Last sequence update)
 GN 15-JUN-2002 (Rel. 41, Last annotation update)
 OS Osmolarity two-component system protein SLN1 (EC 2.7.3.-).
 GN SLN1 OR YP02 OR YIL147C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / YPH1;
 RX MEDLINE=94024010; PubMed=8211183;
 RA Ota I.M., Varshavsky A.;
 RT "A yeast protein similar to bacterial two-component regulators.";
 RL Science 262:566-569(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Genes S., Hamlyn N., Horneill T.S., Hunt S., Jagsis K., Jones M.,
 RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
 RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.

RN [3]
 RP MUTAGENESIS OF HIS-576 AND ASP-1144.
 RX MEDLINE=94239498; PubMed=8183345;
 RA Maeda T., Wurgler-Murphy S.M., Salto H.;
 RT "A two-component system that regulates an osmosensing MAP kinase
 cascade in yeast.";
 RL Nature 369:242-245(1994).
 CC - FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
 CC SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE
 CC EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK2->
 CC PBS2->HOG1 PATHWAY. INACTIVE SLN1 ALLOWS THE UNPHOSPHORYLATED SSK1
 CC PROTEIN TO ACTIVATE SSK2 AND SSK2, TWO MARKERS THAT FURTHER
 CC STIMULATE THE PBS2-HOG1 MAPK CASCADE. IN LOW OSMOLARITY MEDIA,
 CC THE ACTIVATED SLN1 HISTIDINE KINASE REPRESENTS THE ACTIVATION OF THE
 CC PBS2-HOG1 KINASE CASCADE THROUGH PHOSPHORYLATION OF SSK1.
 CC - SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC - PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
 CC BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER
 CC DOMAIN.
 CC - SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC - SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
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DR EMBL: 238059; CAA6131.1; -
 DR EMBL: 001835; AAC48912.1; -
 DR PIR: S48888; S48888.
 DR HSP: P06143; IUDR.
 DR SGD: S0001409; SLN1.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR004358; Bact_sens_pr_C.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR InterPro: IPR003661; His_kinA.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00072; response_reg.1.
 DR Pfam: PF00512; signal.1.
 DR Pfam: PF02518; HATPase_C.1.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR ProDom: PD000039; Response_reg.1.
 DR SMART: SM00387; HATPase_C.1.
 DR SMART: SM00388; HSKA.1.
 DR SMART: SM00448; REC.1.
 DR PROSITE: PS50109; HIS_KIN.1.
 DR PROSITE: PS50110; RESPONSE_REGULATORY.1.
 KW Sensory transduction; Transferase; Kinase; Phosphorylation;
 KW Transmembrane.
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT DOMAIN 47 333
 FT TRANSMEM 334 354
 FT DOMAIN 355 1220
 FT DOMAIN 1089 1210
 FT MOD_RES 576 576
 FT MOD_RES 1144 1144
 FT CARBOHYD 100 100
 FT CARBOHYD 138 138
 FT CARBOHYD 142 142
 FT CARBOHYD 181 181
 FT CARBOHYD 224 224
 FT CARBOHYD 272 272
 FT MUTAGEN 576 576
 FT MUTAGEN 891 891
 FT MUTAGEN 1144 1144
 SO SEQUENCE 1220 AA; 134434 MW; 45FEE24A8165466B CRC64;

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:08:23 ; Search time 28 Seconds

(without alignments)
2663.895 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1863

Sequence: 1 MASLIGTALLAATLAPGGA.....VELVAIVNPSALSSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VIRTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	12	Q67645
2	164	8.8	420	12	Q39309
3	162.5	8.7	354	12	Q98VNI
4	158	8.5	420	12	Q55525
5	156	8.4	384	12	Q69357
6	154	8.3	384	12	Q66931
7	152	8.2	355	12	Q69615
8	149	8.0	355	12	Q69287
9	148	7.9	364	12	Q9YPA1
10	148	7.9	364	12	Q41525
11	147	7.9	259	12	Q91335
12	145	7.8	370	12	Q66789
13	140.5	7.5	369	12	Q91E39
14	139.5	7.5	382	12	Q39505
15	130.5	7.0	366	12	Q99F67
16	125	6.7	356	12	Q88524

17	124.5	6.7	683	12	Q36401	Q36401 alcelaphine
18	123	6.6	355	12	Q67638	Q67638 gallid herp
19	115	6.2	433	11	Q55054	Q55054 mus musculu
20	115	6.2	457	11	Q61396	Q61396 mus musculu
21	108.5	5.8	319	5	Q9M357	Q9M357 drosophila
22	106.5	5.7	235	12	Q9DY19	Q9DY19 bovine herp
23	103	5.5	982	5	Q9VIG1	Q9VIG1 drosophila
24	102.5	5.5	378	4	Q96H15	Q96H15 homo sapien
25	102.5	5.5	4498	5	Q9M223	Q9M223 drosophila
26	99	5.3	279	9	Q9U474	Q9U474 caenorhabdi
27	98	5.3	1011	5	Q9NR29	Q9NR29 heliooverpa
28	97.5	5.2	1714	5	Q9M1X4	Q9M1X4 drosophila
29	96.5	5.2	814	13	Q91897	Q91897 xenopus lae
30	96	5.2	877	4	Q9H306	Q9H306 homo sapien
31	96	5.2	878	4	Q9H307	Q9H307 homo sapien
32	96	5.2	957	4	Q14651	Q14651 homo sapien
33	96	5.2	1217	4	Q9UKW9	Q9UKW9 homo sapien
34	95.5	5.1	332	12	Q8V0L9	Q8V0L9 equine herp
35	95.5	5.1	337	12	Q8V0M1	Q8V0M1 equine herp
36	95.5	5.1	342	12	Q8V0L8	Q8V0L8 equine herp
37	95.5	5.1	356	12	Q8V0L7	Q8V0L7 equine herp
38	95.5	5.1	357	12	Q8V0M2	Q8V0M2 equine herp
39	95.5	5.1	372	12	Q8V0M3	Q8V0M3 equine herp
40	95.5	5.1	374	12	Q8V0L6	Q8V0L6 equine herp
41	95.5	5.1	389	12	Q8V0M0	Q8V0M0 equine herp
42	95.5	5.1	826	12	Q8V0L5	Q8V0L5 equine herp
43	95.5	5.1	867	12	Q39782	Q39782 equine herp
44	95	5.1	745	9	Q9VYU8	Q9VYU8 drosophila
45	95	5.1	1844	5	Q22579	Q22579 caenorhabdi

ALIGNMENTS

RESULT 1	ID	Q67645	PRELIMINARY:	PRT:	362 AA.
AC	Q67645				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	Glycoprotein 1.				
OS	Gallid herpesvirus 1.				
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
OC	Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.				
OX	NCBI_TaxID=10386;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-USDA CHALLENGE STRAIN;				
RX	MEDLINE-9703380; PubMed-8879127;				
RA	Wild M.A., Cook S., Cochran M.;				
RT	"A genomic map of infectious laryngotracheitis virus and the sequence				
RT	and organization of genes present in the unique short and flanking				
RT	regions."				
BL	Viruses Genes 12:107-116(1996).				
DR	EMBL: U28832; AAC55101.1; -				
DR	InterPro: IP002874; Herpes-g1.				
DR	Protein: P01688; Herpes-g1; 1.				
SO	Feature: F01688; Herpes-g1; 1; F530C1AFTCCBAA5 CMC64;				
SO	SEQUENCE 362 AA; 59750 MW; F530C1AFTCCBAA5 CMC64;				
QY	Query Match	100.0%;	Score 1863;	DB 12;	Length 362;
QY	Best Local Similarity	100.0%;	Pred. No. 1.3e-160;		
QY	Matches 362;	Conservative	0;	Mismatches	0;
QY				Indels	0;
QY				Gaps	0;
QY	1 MASLIGTALLAATLAPGANGIVITGNHVSARIDDDHIVVAPPEATIQLOLEFPQ 60				
QY	1 MASLIGTALLAATLAPGANGIVITGNHVSARIDDDHIVVAPPEATIQLOLEFPQ 60				
QY	1 RPKHPYSGVRAFAFSDITNOCYOLSEEFENCTHRSRVGCKVETFFSASNLRTG 120				
QY	1 RPKHPYSGVRAFAFSDITNOCYOLSEEFENCTHRSRVGCKVETFFSASNLRTG 120				
QY	1 RPKHPYSGVRAFAFSDITNOCYOLSEEFENCTHRSRVGCKVETFFSASNLRTG 120				
QY	1 RPKHPYSGVRAFAFSDITNOCYOLSEEFENCTHRSRVGCKVETFFSASNLRTG 120				
QY	121 PPHPEKLTIRNPNDSGMFYIVRLDPTKEPIDVPAIOLSVYQAPNTAATRGVYSKASC 180				

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Db 121 PPHFKLTIRNPNDGMYIVRLDDTKEPIDVFAIQLSVGFAMTAIRGLYSKASC 180
QY 181 RTGCLPTVQLEAVLRTESNRNQAVYATATTSATPTPTATTSASELEAHEHTFP 240
Db 181 RTGCLPTVQLEAVLRTESNRNQAVYATATTSATPTPTATTSASELEAHEHTFP 240
QY 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGLVIVISIVTRNCTP 300
Db 241 WLENGVDHYEPTPANENSNTVRLGTMSPTLIGVTAAVVSATIGLVIVISIVTRNCTP 300
QY 301 HRKLDIVYSDDEERSQTRRSRKGPMVACEINKGADQDSEIVEIVAVSPALSSPDSI 360
Db 301 HRKLDIVYSDDEERSQTRRSRKGPMVACEINKGADQDSEIVEIVAVSPALSSPDSI 360
QY 361 KM 362
Db 361 KM 362
```

RESULT 2

```
039309 PRELIMINARY; PRT; 420 AA.
AC 039309;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Counterpart of HSV-1 gene US7 and VZV gene 67.
GN 73.
OS Equine herpesvirus 4.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_Taxid=10331;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RX MEDLINE=98264497; PubMed-9603335;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-4."
RL J. Gen. Virol. 79:1197-1203(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=NS80567;
RA Telford E.A., Watson M.S., Perry J., Cullinane A.A., Davison A.J.;
RL Submitted (OCT-1997) to the EMBL/Genbank/DBU databases.
DR EMBL; AF030027; AAC59593.1;
DR InterPro: IPR002874; Herpes-g1.
DR Pfam: PF01688; Herpes-g1.
SQ SEQUENCE 420 AA; 45710 MW; 1EB944825DF3D852 CRC64;
```

Query Match 8.8%; Score 164; DB 12; Length 420;
Best Local Similarity 25.5%; Pred. No. 1.8e-06;
Matches 96; Conservative 50; Mismatches 143; Indels 88; Gaps 21;

```
QY 10 LAAATLAPGAMGIVTGNHVSARIDDDHIVYAPREAIQL-QLFEMGQR-PHKRYS 67
Db 13 LLAISMCC--ATAIIRGEHMSMYLNASSEFAVYPRKDSLVVGHMLFDGQGLPTTNS 69
QY 68 GTVAVAFRSDITNOCYOELSEERFENCOTHRSSSVFVGC--KTEYTFEFSNRLTGPHP 125
Db 70 GULEL-IHNHNSKGCYSVIGTISYESCPRVANNAFRSCLHKTSNNHODTFHVVTSETNV 128
QY 126 KLTIRNPNDGMYIVRLDDTKEPIDVFAIQLSVGF--ANTAATRGLYSKASCRFG 184
Db 129 LNIITFPQADSGAYILRLKLNHA-PTADVFGSAFVYDLQSNVTPEVPYPAKEPSNVPT 187
QY 185 LPTVQLEALRTESNRNQAVYATATTSATPTPTATTSASELEAHEHTFPW 241
Db 188 RPPAPAPATSTK-----TGSNTTSSQSTLWYPTP-----RPA 221
QY 242 LENGVDHYEPTPANEN--SNVTVRL-----GTMSPT-----LIGVTAAVVSATIG-- 285
Db 222 LET---HLTTAANETVYSGDTAMLCGFRPSTIAYPTIYMLGLT-----GNLPE 269
```

```
QY 286 --LIVIVISIVTRNCTPHRKLDIVS-----QDDEERSQTRRSR-KRPMY---ACEIN 333
Db 270 DVLIEDESELLR--FPKPKQDTSSRTBEDDFQKQNTSPKSNKLVAAVVIPTACVLM 326
QY 334 KGADQDSEIVEIVAVN 350
Db 327 -----LLVVGAIIN 337
```

RESULT 3

```
098VN1 PRELIMINARY; PRT; 354 AA.
AC 098VN1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE ORF67.
OS Human herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_Taxid=10335;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RX MEDLINE=21109116; PubMed-11162813;
RA Faga B., Maury W., Bruckner D.A., Grose C.;
RT "Identification and Mapping of Single Nucleotide Polymorphisms in the Varicella-Zoster Virus Genome."
RL Virology 280:1-6(2001).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-32;
RA Cole N.L., Faga B.P., Grose C.;
RL Submitted (OCT-2000) to the EMBL/Genbank/DBU databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=VZV-VIA;
RA Grose C., Faga B.;
RT "Identification and mapping of single nucleotide polymorphisms in the Varicella-zoster virus genome."
RL Submitted (DEC-2000) to the EMBL/Genbank/DBU databases.
DR EMBL; AF314221; AKK19249.1;
DR EMBL; AF325441; AKK01055.1;
DR InterPro: IPR002874; Herpes-g1.
DR Pfam: PF01688; Herpes-g1.
SQ SEQUENCE 354 AA; 39373 MW; 3F01739F3AFC6B08 CRC64;
```

Query Match 8.7%; Score 162.5; DB 12; Length 354;
Best Local Similarity 22.4%; Pred. No. 2e-06;
Matches 72; Conservative 53; Mismatches 111; Indels 85; Gaps 15;

```
QY 23 IVTGNHVSARIDDDHIVYAPRE--ATIQQLFFMGQR-HKRYSGVAVAFRSDI 78
Db 21 LIRKGDHVSILQVNSLSTLIPQNDNYTEIKQLVFIQDLGTGNYSGTELLT-ADT 79
QY 79 TNOCYOELSEERFENCOTHRSSSVFVGCYV---EYTFEFSNRLTGPHPFKLTIRNRP 135
Db 80 VAFCEFSVQVIRDQCPRIRTSAFISCRKHSNHYGNSIDRISTERDAGVMLKITRPGIN 139
QY 136 DSGMFIYVRLDDTKEPIDVFAIQLSVY-----QFANTAATRGLYSKAS 179
Db 140 DAGVYVLLVRLDHSRS-TDGFILGVNVYVAGSHNHIGVITYTSPSLQNGYSTRALFQA- 197
QY 180 CRTFGIPT-----VQLEAVLRTES--WRNQAVYATATTSATPTPTPT 225
Db 198 -RUCDIPATPKSGTSLFQHMLDLRAGKSLDNPMLH-EDVVTTERKSVYKKG----- 248
QY 226 ATSASELEAHEHTFPLWLENGVDHYEPTPAN--ENS-----NVTVRLGTMSPTLIGTV 276
Db 249 -----IEN--HYVPTKSTLPKSLNDPKNLLI-----IIPYIA 281
QY 277 AAVVSATIGLVIVISIVTRNM 297
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Dd	282	SVMLTAAVIVIVISVKRRKI	302
RESULT 4	:	: :	:
AC	055525;	PRELIMINARY;	PRT; 420 AA.
Dt	01-JUN-1998 (TREMBLEJ. 06, Created)		
Dt	01-JUN-1998 (TREMBLEJ. 06, Last sequence update)		
Dt	01-JUN-2001 (TREMBLEJ. 17, Last annotation update)		
Dd	Glycoprotein I homologue.		
Dd	Equine herpesvirus 4.		
Dd	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Varicellovirus.		
NCBI_TaxID=10331;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
KC	STRAIN-TN20;		
DR	MEDLINE=98185635; PubMed=9524947;		
DR	Damini A.M., Matsumura T., Yokoyama N., Maeda K., Miyazawa T.,		
Ra	Kai C., Mikami T.;		
RT	"Nucleotide sequences of glycoprotein I and E genes of equine		
RL	herpesvirus type 4."		
J. Vet. Med. Sci.	60:219-225(1998).		
EMBL: AB005749; BAA25021.1;			
Interp. IPB002874; Herpes-GI.			
Fram: PF01688; Herpes-GI. 1-			
SOURCE	420 AA; 45696 MW, 1f64F5E179CZD916 C664;		
Query Match	8 5%; Score 158; DB 12; Length 420;		
Best Local Similarity	25.5%; Pred. No. 6,4e-06;		
Matches	96; Conservative 49; Mismatches 144; Indels 88; Gaps		
OY	10 LLAATLAPGAGCIYITGNHVSARIDDDHVIVAPRAPATIO-QLFPMQGR-PHKRYS 67		
Dd	13 LLAISMCK--AAILYRGESMSMTLNSSFPAYVRKDKSLVYGHHMFLDGRIPTTNYS 69		
OY	68 GTVAFAFRSDITNOCIOELSERPENCSTRHSSEVYGC--KVETFYFSASNKLTGPPIHF 125		
Dd	70 GLIEL-LHNWYSGCCSVIOGTISTESCPRVANNARRSCLIKTSNHNDIFHNVTSEYNV 128		
OY	126 KLTRINRPDSGMETVIVLRDDTKEPIDVFALQISVYQF-AHTAATRLGLSKASCRTFG 184		
Dd	129 LLNTTWOPADSCAVTLARKLNHA-PRADFEGSAFVDLOSNTVPPEPVTAKEPSNVFT 187		
OY	185 LPVQLFAVLRYTEESWRMQAVYVATEATTTSBAT--TPPVATTSASELEAHETFEW 241		
Dd	188 RTPAAPAANSTK-----TGSNITSOSGYLYTPP-----RPA 221		
OY	242 LENGVDFEPTPPANEN--SNVTYRL-----GTMSPT-----LIGTYAAVVASATIG--- 285		
Dd	222 LET---HLTTAPANEIVVSGDTAMLCGFSPSTAFTYMILGLT-----CNLPE 269		
OY	286 --LVTVSIYTRMKCPHRKKLDVTSODE-----ERSQTRESR-KFGPNV-----ACEIN 333		
Dd	270 DVLIIHEDEIR---TPPKPQTTSSRTEDDAFKOTNSTSPKSRNKIVAAVVIPTCACYLM 326		
OY	334 KGADQDELVELVAIVN 350		
Dd	327 -----LLTVVGAIIN 337		
RESULT 5			
ID	069357	PRELIMINARY;	PRT; 384 AA.
AC	069357;		
Dt	01-NOV-1996 (TREMBLEJ. 01, Created)		
Dt	01-NOV-1996 (TREMBLEJ. 01, Last sequence update)		
Dt	01-JUN-2001 (TREMBLEJ. 17, Last annotation update)		
Dd	Homologue of HSV-1 gI.		
Dd	Feline herpesvirus (field herpesvirus 1).		
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		

[illegible]

Query Match	8.3%	Score 154	DB 12	Length 384
Best Local Similarity	22.3%	Pred. No. 1.3e-05		
Matches 73	Conservative 52	Mismatches 133	Indels 70	Gaps 13
OY	5	LCITLLAATLTPFCGAMGIVITGNHVSATIDDDHIYVAPRE-ATIQQLFFPMGO--RP	62	
DB	1	MSIAFIYILMAIGVYIGVYRGDHSLSHVDTSSGFVIPTLENTIYCHLFLDDP	60	
OY	63	HKRPQVAVAFRSDITNOCYQELSEERFENCTHRSSSVFVC--KVTEYTSASRLNG	120	
DB	61	VANNNGTLEI-ITHYNNHSSCYKIQVIEYSSCPVRNNNAFRCLKHTSMHQDQSLIMTS	119	
OY	121	PPHFKLITRNRPDSCGFYIYALDPTKEIDVFAIDLSYYQANATATGLYSKASC	180	
DB	120	VETGMLLTITTSFKMDGGIYALRVRFNNHK--ADVEGLSVFYSF---DTGRGHRHMADE	174	
OY	181	RTFGV--LPTVQ--LEAYLRTESRMNQAV---VATEATTSAEATTPPVATTSASELBA	234	
DB	175	NUNGELITTPSPMEYIKVY-----NTPYIDHAWTTQTTSNKSMESEPSVTSISC-----	223	
OY	235	EHFTEPMELENGVDHPEPTPANENSNTVRL-----GTMSPTLIGYVAA	278	
DB	224	-----HFEQNDPNEGELTLYTHLNIAGNITVDVWMDGTLKPLRIMDGLNL	270	
OY	279	VYSAT-----ICGLYIYSTI 292		
DB	271	SVTSSFKNETTQCKMTPDRKVFYIVISI 298		
RESULT 7				
OY	09E6L5	PRELIMINARY	PRT	355 AA.
AC	09E6L5			
DT	01-MAR-2001 (TREMBlrel. 16, Created)			
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)			
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)			
DE	US7 membrane glycoprotein I-like protein.			
GN	MDV095			
OS	Turkey herpesvirus.			
OC	Viruses: dsDNA viruses, no RNA stage: Herpesviridae;			
OC	Alphaherpesvirinae; Marek's disease-like viruses.			
OX	NCBI_TaxID=10390;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MDS:			
RX	MEDLINE=20392152; PubMed=10933706;			
RA	Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF243438; AAC14268.1;			
DR	InterPro: IPR002874; Herpes_gf.			
DR	Pfam: PF01688; Herpes_gf; 1-gf.			
SO	SEQUENCE 355 AA; 40568 MW; D23A6DA126ACDB00 CAC64;			
Query Match	8.2%	Score 152	DB 12	Length 355
Best Local Similarity	22.9%	Pred. No. 1.8e-05		
Matches 78	Conservative 55	Mismatches 166	Indels 42	Gaps 14
OY	19	GAMGIVITGNHVSATIDDDHIYVAPRE-ATIQQLFFPMGOQPHAKYSGTVAVAFSD	77	
DB	15	GIWSTIVYGTSTJLSDSALVAFEGGLDKMVAVRQQLFLGDQRTSSYTGTTEI-LKWD	73	
OY	78	ITNOCYQELSEERFENCTHRSSSVFVCKVTEYTSASRLNGRPHPK---LITRNRP	134	
DB	74	EYKCYSTVLHATSYNDCALDAIVRGCRDAVVYAQPHDRV--OPFEKGTLLKIVPRV	131	

QY	135	NSGSEFYVYRLDDKPEPFDVAIQOLSVQFANTATRLVYKASCRTEGCLPVOLEATL	194
QY	135	NSGSEFYVYRLDDKPEPFDVAIQOLSVQFANTATRLVYKASCRTEGCLPVOLEATL	194
Db	132	SDTGSYIRVVALAG-RNMSDIFRMVAIIIS-----SKSMACNHSASSFOAHKCI	179
QY	195	PTEE--SWRMQOAVYATEATTSAEATPTPYATASASELEAHEFTPMLENGVDHDEPT	252
Db	180	KVDMRAEFENYILIGHVGNLDDSDSELHAIYNTTPOS-TDINIITTPPYDNGSTIYSP	238
QY	253	P--ANENSNTVRLGT-MSPTLIGVYAAV--SATIGLVIV--ISIVTRNCTPHRK	303
Db	239	VENLENNNSHVDMAMSTGMGMTVLKYTLPRLLYFSMTVIYLCIALAIYLCERCNSPHRR	298
QY	304	LDTVSODDEERSQTRRESKRFQPMVACEINKADDSOLVE	344
Db	299	I---YIGEPKRSDE-----APLITSAVNESFOYDYNKE	328
RESULT 8			
ID	Q69287	PRELIMINARY:	PRT: 355 AA.
AC	Q69287;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DI	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	Membrane glycoprotein 1 precursor.		
GN	US7.		
OS	Turkey herpesvirus.		
CC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
OC	Alphaherpesvirinae; Marek's disease-like viruses.		
OX	NCBI_TaxID=10390;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95133166; PubMed=7831788;		
RA	Brunovskis P., Velicer L.F.;		
RT	"The Marek's disease virus (MDV) unique short region:		
RT	alphaherpesvirus homologous, fowlpox virus homologous, and MDV-		
RT	specific genes."		
RL	Virology 206:324-338(1995).		
DR	EMBL; L212174; AAA64968.1;		
DR	InterPro: IPR002874; Herpes_g1.		
-DR	Pfam: PF01688; Herpes_g1.1.		
KW	Signal.		
FT	SIGNAL 1 18 POTENTIAL.		
FT	CHAIN 19 355 MEMBERANE GLYCOPROTEIN I.		
SO	SEQUENCE 355 AA; 40579 MW; 40CD25034E4EAE6F CRC64.		
Query Match 8.0%; Score 149; DB 12; Length 355;			
Best Local Similarity 23.3%; Pred No. 1.3e-05;			
Matches 80; Conservativity 54; Mismatches 163; Indels 46; Gaps 15			
QY	19	GAMGIVITGNHNSARIDDDHIVAVPR--PEATIQLOLFEPGPGRPKPKPSGYAVAVAR	75
Db	15	GIMSIYVGTSTVT--LSTDQSALVAFRGDKKVVNVRGQLFLGDQTRTSYGTTEI-LK	71
QY	76	SDITMOQOELSEEPFENCNTHRSSSVFYGCCKATYETTFSSANLITGPAPHFK---LTIRNP	132
Db	72	WDEEKYCSVLTATSYMCCPAIDAFVFRCCRAVVAOAPHGV--QPFPEKGTLLRIYEP	129
QY	133	RPNDSGMFPVYIRLDDTKEPIDVPAIQOLSVQFAMTAATRGVYKASCRTEGCLPVOLEA	192
Db	130	RVSDDGYIIRVSLAG-RNMSDIFRMVAIIIS-----SKSMACNHSASSFOAHK	177
QY	193	YLRTPE--SWRMQOAVYATEATTSAEATPTPYATASASELEAHEFTPMLENGVDHDE	250
Db	178	CIRYVDRAFAEFYLLIGHVGNLDDSDSELHAIYNTTPOS-TDINIITTPPYDNGSTIY	236
QY	251	PTP--ANENSNTVRLGT-MSPTLIGVYAAV--SATIGLVIV--ISIVTRNCTPH	301
Db	237	PTVENLNNNSHVDMAMSTGMGMTVLKYTLPRLLYFSMTVIYLCIALAIYLCERCNSPH	296
QY	302	RKLDTVSODDEERSQTRRESKRFQPMVACEINKADDSOLVE	344
Db	297	RRI---YIGEPKRSDE-----APLITSAVNESFOYDYNKE	328

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RESULT 9
OYPAI ID OYPAI PRELIMINARY: PRT: 364 AA.
AC OYPAI:
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Similar to HSV-1 gT.
OS Canine herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae.
OX NCBI_TaxID=37110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSL-2;
RA MEDLINE=98185505; PubMed=9524817;
RA Tyack S.G., Studdert M.J., Johnson M.A.;
RA "Nucleotide sequence of canine herpesvirus homologues of herpes
RT simplex virus type 1 US2, US3, glycoproteins I and E, US8.5 and US9
RT genes."
RL DNA Seq. 7:365-368(1997).
DR EMBL: U49380; AAC67213.1;
DR InterPro: IPR002874; Herpes_gT.
DR Pfam: PF01688; Herpes_gT.1.
DR SMART: SM00034; CLECT.1.
SQ SEQUENCE 364 AA: 41999 MW: B9EC33EE7FB913A9 CRC64:

Query Match 7.9% Score 148; DB 12; Length 364;
Best Local Similarity 27.3%; Pred. No. 4.2e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

OY 4 LIGTALLAATLAPGANGIVITGNHVSARIDDDHIVYVAPREPTATQQLFPMGQR-P-62
DB 16 LITMFLPTLFLFYGVNGFYKGYISMLNTSSGFSIFPDDKFIYSGRLFLDDQHL 75
OY 63 HKPYSGTVAVAFRSDITNOCYOELSEBERENCTHRSSSVFVGC--KVTEYTFASNRLTG 120
DB 76 VNNYSGTIEFI---HFNNSCYTYOTIEYFSCPRIFNNAFSCCLKVKSHESQLRINSS 132
OY 121 PPHPEKLTIRNRPNDSCMFYIVRLDDTKREPIDVFAIQLSVYOF 165
DB 133 IENGVLLEITNPKPNDSCGVYFIRVQLENNK--TDVFGIPAFIYSF 175

ULT 10
525
O41525 PRELIMINARY: PRT: 364 AA.
AC O41525:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CUS7 (glycoprotein I).
GN GI.
OS Canine herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae.
OX NCBI_TaxID=37110;
RN [1]
RP SEQUENCE FROM N.A.
RA Haanes E.J., Tomlinson C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=YPI110;
RA MEDLINE=98453388; PubMed=9784067;
RA Nishikawa Y., Xuan X., Otsuka H.;
RT "Identification and characterization of the glycoprotein E and I genes
RT of canine herpesvirus."
RL Virus Res. 56:77-92(1998).
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=AUSSTRALIAN;
RA Reubel G.H., Pekin J., Webb-Magg K., Hardy C.M.;
RT "Nucleotide sequence of glycoprotein genes B, D, G, H and I, thymidine
RT kinase and protein kinase genes and gene homologue UL 24 of an
RT Australian isolate of canine herpesvirus."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U84223; AB67059.1;
DR EMBL: AB003728; BAA33765.1;
DR EMBL: AF361076; BAA31063.1;
DR InterPro: IPR002874; Herpes_gT.
DR Pfam: PF01688; Herpes_gT.1.
DR SMART: SM00034; CLECT.1.
SQ SEQUENCE 364 AA: 42068 MW: 08EC32E7FB913A8 CRC64:

Query Match 7.9% Score 148; DB 12; Length 364;
Best Local Similarity 27.3%; Pred. No. 4.2e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

OY 4 LIGTALLAATLAPGANGIVITGNHVSARIDDDHIVYVAPREPTATQQLFPMGQR-P-62
DB 16 LITMFLPTLFLFYGVNGFYKGYISMLNTSSGFSIFPDDKFIYSGRLFLDDQHL 75
OY 63 HKPYSGTVAVAFRSDITNOCYOELSEBERENCTHRSSSVFVGC--KVTEYTFASNRLTG 120
DB 76 VNNYSGTIEFI---HFNNSCYTYOTIEYFSCPRIFNNAFSCCLKVKSHESQLRINSS 132
OY 121 PPHPEKLTIRNRPNDSCMFYIVRLDDTKREPIDVFAIQLSVYOF 165
DB 133 IENGVLLEITNPKPNDSCGVYFIRVQLENNK--TDVFGIPAFIYSF 175

RESULT 11
OY 091335 PRELIMINARY: PRT: 259 AA.
AC 091335:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE Glycoprotein I.
OS Canine herpesvirus.
OC Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
OC Alphaherpesvirinae.
OX NCBI_TaxID=37110;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DFD-6;
RA MEDLINE=98453388; PubMed=9784067;
RA Nishikawa Y., Xuan X., Otsuka H.;
RT "Identification and characterization of the glycoprotein E and I genes
RT of canine herpesvirus."
RL Virus Res. 56:77-92(1998).
DR EMBL: AB003728; BAA33764.1;
DR InterPro: IPR002874; Herpes_gT.
DR Pfam: PF01688; Herpes_gT.1.
DR SMART: SM00034; CLECT.1.
SQ SEQUENCE 259 AA: 29965 MW: 66C7A9A957FF7E0F CRC64:

Query Match 7.9% Score 147; DB 12; Length 259;
Best Local Similarity 27.3%; Pred. No. 3.3e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

OY 4 LIGTALLAATLAPGANGIVITGNHVSARIDDDHIVYVAPREPTATQQLFPMGQR-P-62
DB 16 LITMFLPTLFLFYGVNGFYKGYISMLNTSSGFSIFPDDKFIYSGRLFLDDQHL 75
OY 63 HKPYSGTVAVAFRSDITNOCYOELSEBERENCTHRSSSVFVGC--KVTEYTFASNRLTG 120
DB 76 VNNYSGTIEFI---HFNNSCYTYOTIEYFSCPRIFNNAFSCCLKVKSHESQLRINSS 132
OY 121 PPHPEKLTIRNRPNDSCMFYIVRLDDTKREPIDVFAIQLSVYOF 165

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Db 133 IENGVLLEITNPKRNDGCVFIRVOLENNK--TDVFGIPAFVYSF 175

RESULT 12

ID 086789 PRELIMINARY: PRT: 370 AA.

AC 086789;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glycoprotein gi.

OS feline herpesvirus (field herpesvirus 1).

OC viruses: dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicellovirus.

OX NCBI_Taxid=10334;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94267406; PubMed=8207390;

RA Spatz S.J., Kota P.A., Maes R.R.;

"Identification of the feline herpesvirus type 1 (FHV-1) genes encoding glycoproteins G, D, I and E: expression of FHV-1 glycoprotein D in vaccinia and raccoon poxviruses.";

J. Gen. Virol. 75:1235-1244(1994).

RL EMBL: S72415; AAB30961.1;

DR Interpro: IPR002874; Herpes_gi: 1.

DR Pfam: PF01688; Herpes_gi: 1.

SQ SEQUENCE 370 AA: 41568 MW: 2A816ECB37466A77 CRC64;

Query Match 7.8%; Score 145; DB 12; Length 370;

Best Local Similarity 22.0%; Pred. No. 8.1e-05;

Matches 72; Conservative 52; Mismatches 136; Indels 68; Gaps 14;

QY 5 LGTLALATLAFPGAMGIVITGNHVSARIDDDHIVAPRP-ATIQQLFPMPCQ-RP 62

Db 1 MSIATVILMAIGYVYRGDHWSLNHDTSSEGVYPTLENTIIGLILDDQPLP 60

QY 63 HKYSGTVKAFPSDITNOCYOLSEERENCNHRSSSVFVGC--KVTEYTFASNRLTG 120

Db 61 VNNYNGTLEI-INYHNSCYKIVQVIEYSSCPVRNNAFRSCLHNTSMHQYDLSINTS 119

QY 121 PRHPFLITRNPRNDGCVFIRVOLENNK--TDVFGIPAFVYSF 175

Db 120 VERGMLLTITSPKMDGGLIALNVRNNHNNK-ADVFGLSVYFSF----DFGRHHHDE 174

QY 181 RTFG--LPTVQ--LEAYLRTEESWRNMQAY--VATEATTSATPTPTVATASLEA 234

Db 175 NLNGEILITPSPMETVVKV----NTPYDHWYTTQTTSKMSSEPSNTSISC-----223

QY 235 EHRTFPMLENGVDHYEPTANENSNTVRL-----GYSPTLIGVTVA 278

Db 224 -----HTPQNDPNEGETLYTHLNTAGNITYDVMVMDGTTLKPRLI-----264

QY 279 VVSATIGLVIVISITVRNMCTPHRKLDT 306

Db 265 ----DMGLNLSTVSSFKK--GNHAKMDT 286

RESULT 13

ID 091E39 PRELIMINARY: PRT: 369 AA.

AC 091E39;

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Glycoprotein I.

GN US7

OS Phocid herpesvirus 1.

OC viruses: dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicellovirus.

OX NCBI_Taxid=47418;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PB84;

RA Martina B., Osterhaus A.D.M.E., Harder T.C.;

RT "Identification and analysis of immunogenicity of the glycoprotein D equivalent within the unique short segment of phocid herpesvirus-1.";

RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ290955; CAC51466.1;

DR Interpro: IPR002874; Herpes_gi: 1.

DR Pfam: PF01688; Herpes_gi: 1.

SQ SEQUENCE 369 AA: 42372 MW: 1587181704A7A8A CRC64;

Query Match 7.5%; Score 140.5; DB 12; Length 369;

Best Local Similarity 25.1%; Pred. No. 0.00021;

Matches 57; Conservative 36; Mismatches 89; Indels 45; Gaps 10;

QY 22 GIYTGNGHVSARIDDDHIVAPRP-EATIQQLFPMPCQ-RPHKPYSGTVKAFPSDIT 79

Db 16 GIYRGTYKSMYVNTSSGVYVYDDDFNTGVLGLLDDQRLPVTNYSGLIEITY----FN 72

QY 80 NCCYOLSEERENCNHRSSSVFVGC--KVTEYTFSA---SNRLGPPHPFLITRNPR 133

Db 73 YSCYTYVQTEYVSCPRHNNNAFRSCLIKVSKHQSLRINSIENG----VLEIKNPK 128

QY 134 PNDGCVFIRVOLENNK--TDVFGISAFVYSFVSKSG--ENITKPDSENQ-----173

Db 129 PSDSGVYIFRVOLENNK--TDVFGISAFVYSFVSKSG--ENITKPDSENQ-----173

QY 194 LRTEESWRNMQAYVATEATTSALAE-----TTPPTVATASLE 232

Db 174 -----ENFTNHLVPTSTITKPSSESHLNTFTPTDIPAPVCHV 213

RESULT 14

ID 039505 PRELIMINARY: PRT: 382 AA.

AC 039505;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glycoprotein I.

GN US7

OS Bovine herpesvirus 1.

OC viruses: dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Varicellovirus.

OX NCBI_Taxid=10320;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JURA;

RA Goltz M., Buhk H.J., Broil H., Lewin M., Mankertz A., Boerner B., Borchers K., Weigelt W.;

RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE OF 372-382 FROM N.A.

RC STRAIN=JURA;

RA Schwyzer M.;

RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=JURA;

RA Schwyzer M., Paces V., Letchworth G.J., Misra V., Buhk H.J., Lowery D.E., Simard C., Bello L.J., Thiry E., Vlack C.;

RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=COOPER;

RA Goltz M., Buhk H.J., Schwyzer M.;

RT "Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome.";

RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ004801; CAA06146.1;

DR EMBL: Z98199; CAB10890.1;

DR Interpro: IPR002874; Herpes_gi: 1.

DR Pfam: PF01688; Herpes_gi: 1.

SQ SEQUENCE 382 AA: 39596 MW: 0F06C95CD2581EC2 CRC64;

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:14:43 : Search time 16.5 Seconds
(without alignments)
1893.078 Million cell updates/sec

Title: US-09-993-777-7

Perfect score: 1863

Sequence: 1 MASLIGTALIAATLAPFGA.....VEIVAIYVPSALSPDSIKM 362

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328255 seqs, 8628685 residues

tal number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications: AA:*
1: /cgn2.6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2.6/ptodata/2/pubppaa/PCOT_NEW_PUB.pep.*
3: /cgn2.6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2.6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2.6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2.6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2.6/ptodata/2/pubppaa/PCOTUS_PUBCOMB.pep.*
8: /cgn2.6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
9: /cgn2.6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2.6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
11: /cgn2.6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
12: /cgn2.6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
13: /cgn2.6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*
14: /cgn2.6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1863	100.0	362	10	US-09-881-457A-5
2	148	7.9	364	9	US-10-156-275-56
3	115	6.2	612	9	US-10-125-652-10
4	112	6.0	387	9	US-10-114-893-133
5	108	5.8	713	10	US-09-801-368-408
6	102.5	5.5	379	9	US-09-813-153-138
7	97	5.2	1220	10	US-09-801-368-332
8	93	5.0	320	9	US-09-738-626-5621
9	92.5	5.0	547	10	US-09-753-436-1
10	91	4.9	365	9	US-09-870-759-73
11	90.5	4.9	359	9	US-09-978-295A-45
12	90.5	4.9	359	9	US-09-978-697-45
13	90.5	4.9	359	9	US-09-978-192A-45
14	90.5	4.9	359	9	US-09-999-832A-45
15	90.5	4.9	359	9	US-09-978-189-45
16	90.5	4.9	359	9	US-10-174-590-42
17	90.5	4.9	359	9	US-10-176-758-42
18	90.5	4.9	359	9	US-10-175-737-42
19	90.5	4.9	359	9	US-10-173-706-42

20	90.5	4.9	359	9	US-10-175-738-42	Sequence 42, Appl
21	90.5	4.9	359	9	US-10-175-752-42	Sequence 42, Appl
22	90.5	4.9	359	9	US-10-176-482-42	Sequence 42, Appl
23	90.5	4.9	359	9	US-10-176-757-42	Sequence 42, Appl
24	90.5	4.9	359	9	US-10-176-913-42	Sequence 42, Appl
25	90.5	4.9	359	9	US-10-180-557-42	Sequence 42, Appl
26	90.5	4.9	359	9	US-10-180-557-42	Sequence 42, Appl
27	90.5	4.9	359	9	US-10-173-700-42	Sequence 42, Appl
28	90.5	4.9	359	9	US-10-174-576-42	Sequence 42, Appl
29	90.5	4.9	359	9	US-10-174-582-42	Sequence 42, Appl
30	90.5	4.9	359	9	US-10-174-588-42	Sequence 42, Appl
31	90.5	4.9	359	9	US-10-175-739-42	Sequence 42, Appl
32	90.5	4.9	359	9	US-10-175-740-42	Sequence 42, Appl
33	90.5	4.9	359	9	US-10-175-743-42	Sequence 42, Appl
34	90.5	4.9	359	9	US-10-176-488-42	Sequence 42, Appl
35	90.5	4.9	359	9	US-10-176-492-42	Sequence 42, Appl
36	90.5	4.9	359	9	US-10-176-497-42	Sequence 42, Appl
37	90.5	4.9	359	9	US-10-176-750-42	Sequence 42, Appl
38	90.5	4.9	359	9	US-10-176-885-42	Sequence 42, Appl
39	90.5	4.9	359	9	US-10-176-987-42	Sequence 42, Appl
40	90.5	4.9	359	9	US-10-176-991-42	Sequence 42, Appl
41	90.5	4.9	359	9	US-10-176-992-42	Sequence 42, Appl
42	90.5	4.9	359	9	US-10-176-993-42	Sequence 42, Appl
43	90.5	4.9	359	9	US-10-184-658-42	Sequence 42, Appl
44	90.5	4.9	359	9	US-10-173-695-42	Sequence 42, Appl
45	90.5	4.9	359	9	US-10-173-695-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-881-457A-5
Sequence 5, Application US/09881457A
Patent No. US20020081316A1
GENERAL INFORMATION: Mark D
APPLICANT: Cochran, Stephanie M
TITLE OF INVENTION: NO. US0020081316A1el Avian Herpes Virus and Uses Thereof
FILE REFERENCE: ST0105A1QOK
CURRENT APPLICATION NUMBER: US/09/881,457A
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/426,352
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 08/804,372
PRIOR FILING DATE: 1997-02-21
PRIOR APPLICATION NUMBER: PCT/US95/10245
PRIOR FILING DATE: 1995-08-09
PRIOR APPLICATION NUMBER: 08/663,566
PRIOR FILING DATE: 1996-06-13
PRIOR APPLICATION NUMBER: 08/288,065
PRIOR FILING DATE: 1994-08-09
PRIOR APPLICATION NUMBER: PCT/US93/05681
PRIOR FILING DATE: 1993-06-14
PRIOR APPLICATION NUMBER: 08/023,610
PRIOR FILING DATE: 1993-02-26
PRIOR APPLICATION NUMBER: 07/898,087
PRIOR FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 362
TYPE: PRT
ORGANISM: Infectious Laryngotracheitis Virus
US-09-881-457A-5
Query Match: 100.0% Score 1863; DB 10; Length 362;
Best Local Similarity 100.0% Pred. No. 5.5e-166;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MASLIGTALIAATLAPFGAGIYITGNHVSATIDDHIVIVAPPEATLOLOFPMPQ 60
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Db 1 MASLGLTALLATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIOLOLFMPGQ 60
Qy 61 RHPKPSGTVARAFRSDDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTESASNRLTG 120
Db 61 RHPKPSGTVARAFRSDDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTESASNRLTG 120
Qy 121 PPHPRFLTRNRPNDSGMFYIVRLDDTKPEIDVFAIOLSYQFANTATRGYSKASC 180
Db 121 PPHPRFLTRNRPNDSGMFYIVRLDDTKPEIDVFAIOLSYQFANTATRGYSKASC 180
Qy 181 RFFGLPTVOLVAVLRTESRMNOAVVATEATTSAETTPPVATTSASELEHFTFP 240
Db 181 RFFGLPTVOLVAVLRTESRMNOAVVATEATTSAETTPPVATTSASELEHFTFP 240
Qy 241 WLENGVDHTEPTPANENSNTVRLGTMSPTLIGTVAAVSAITGLVIVISITRNMCPT 300
Db 241 WLENGVDHTEPTPANENSNTVRLGTMSPTLIGTVAAVSAITGLVIVISITRNMCPT 300
Qy 301 HRRLOTVSODDERSGTRESRKFQPMVACEINKGADQSELVELVAINPSALSSPDSI 360
Db 301 HRRLOTVSODDERSGTRESRKFQPMVACEINKGADQSELVELVAINPSALSSPDSI 360
Qy 361 KM 362
Db 361 KM 362

RESULT 2
US-10-156-275-56
; Sequence 56, Application US/10156275
; Publication NO. US2003004944A1
; GENERAL INFORMATION:
; APPLICANT: Haanes, Elizabeth J.
; TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,275
; FILING DATE: 28-May-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/399,118
; FILING DATE: <unknown>
; APPLICATION NUMBER: 08/680,726
; FILING DATE: 12-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-46-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 364 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-156-275-56

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Query Match 7.9%; Score 148; DB 9; Length 364;
Best Local Similarity 27.3%; Pred. No. 1e-05;
Matches 45; Conservative 30; Mismatches 82; Indels 8; Gaps 4;

Qy 4 LIGTALLATLAPFGAMGIVITGNHVSARIDDDHIVYAPREATTIOLOLFMPGQ-P 62
Db 16 LITMFLPFLFELVGNDFVYKGYISMFNLNSSGFSIFPDOKFTVSRLLFLDDQHUS 75
Qy 63 HRPYSGTVARAFRSDDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTESASNRLTG 120
Db 76 VNNYSTIEFI---HNNSCYTPYQIIEYFSCRIENNMFRLSKKVSQHHESQULINS 132
Qy 121 PPHPRFLTRNRPNDSGMFYIVRLDDTKPEIDVFAIOLSYQF 165
Db 133 IENGVLLEITNPKRPNDSGVYFIRVQLENNK--TDVGIAPFIYSF 175

RESULT 3
US-10-125-692-10
; Sequence 10, Application US/10125692.
; Publication NO. US2003004429A1
; GENERAL INFORMATION:
; APPLICANT: Aderem, Alan
; APPLICANT: Hayashi, Rumioka
; APPLICANT: Smith, Kelly D.
; APPLICANT: Underhill, David M.
; APPLICANT: Ozlinsky, Adrian
; TITLE OF INVENTION: Toll-Like Receptor 5 Ligands and Methods
; FILE REFERENCE: P-15 5155
; CURRENT APPLICATION NUMBER: US/10/125,692
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/285,477
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-692-10

Query Match 6.2%; Score 115; DB 9; Length 612;
Best Local Similarity 20.6%; Pred. No. 0.026;
Matches 76; Conservative 54; Mismatches 133; Indels 106; Gaps 16;

Qy 19 GAMGIYITNHSARIDDDHIVYAPREATTIOLOLF---FMPGQRPKPSGTVARAF 75
Db 93 GSPFLIT--NKLKMEDSOTYICELNKE--EVELWYFKVTFSGTSLLOGSITLILDSN 149
Qy 76 SDITNOCYOELSEERFENCSTRSSSVFVGCKVTEYTESASNRLTGPPHPRFLTRNRPN 135
Db 150 SKVSN---PLTE---CKHKKGVSGSKV-----LSMSNLRVQ 181
Qy 136 DSGMFYIVRLDDTKPEIDVFAIOLSYQFANTATRGYSKASCRTPLPVQLEAVLR 195
Db 182 DDDFMNCTVTLDDKK---NMFQMTLSVLGFOSYALT-AVKSSESAEFSFPLNFAE--- 233
Qy 196 TEESWRN--WQYVVAATEATTSAETTPPVATTSASELEHFTFPLENGVDHTEPT 253
Db 234 -ENGCELMMKA-----EKSFQPMVAFSISIKKEVSV 265
Qy 254 ANENSNTVRLGTMSPTLIGTVAAVSAITGLVIVISITRNMCPTPRKRLDTVSODDE 313
Db 266 QKSTDLKQLKELPLTLTKIPQVSHQFAGSGL---TLTLDKGLHQEVNLVYKVAQ 321
Qy 314 RSQTRRESKRFQPMVACEIN-----KGAQD---SELVELVAINPSA----- 353
Db 322 LNNI-----LTCEVMGPTSPKRMRLTLQENQEARVSEOKVQVYVABETGLMOCL 371
Qy 354 LSSPDSIKM 362
Db 372 LSEGDVKM 380

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PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: 60/073,170
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 298
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 138
LENGTH: 379
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (379)
OTHER INFORMATION: Xaa equals stop translation
US-09-813-153-138

Query Match
Best Local Similarity 23.6%; Pred. No. 0.2; Length 379;
Matches 73; Conservative 36; Mismatches 133; Indels 67; Gaps 13;

65 PYSGVAVAFRSDITNOCYOELSEERFENCTHRSSVFGCKYETEFSSANRLTG--PP 122
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60 PYSCKEALIRTD-----GMRVTSRK-SAKYRLQGTIPR 92
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QY 123 HPRKLTIRPNRPNDSGMFYIVRL---DDTKRPIDVFAQLSVQFANTATRLGLYSKA 178
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DB 93 GDVSLTILNPESDSGVCCRIEVPGMFNDVK-----INVLNL-CRASTTHTATATTT 146
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QY 179 SCRTFGLPTVQLEAVLRTESMRNMOAYVATEATTSAEATPTP-----VTATSASE 231
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DB 147 RRTTTSPT-----TTRQMTTTPALPTTYVT-PDITGTPIQMTIANFTTANNC 197
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QY 232 LENAHTFPLNGLVGHYEPTPANENSNTVRLGMSPLIGTVAAVVSATIGLVIYIS 291
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DB 198 LSLTPSTLP-EBATGLTPPEPSKGPILTAESEITVLPSSMSAESTSADTILTSKES 255
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QY 292 IYTRNCTPH---RKLDPVQSODEERSOT---RESRRKFGMVACETINKGADOSELY 343
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DB 256 KWDLPSTSHVSMKTSDSVSPQASDTAVPEQNKTKTGQDGC--IPMSKNEMPIIS 313
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QY 344 ELVAIVNPS 352
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DB 314 QLLMITAPS 322
|||

RESULT 7
US-09-801-368-332
Sequence 332, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: NO. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 332

LENGTH: 1220
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match
Best Local Similarity 22.7%; Pred. No. 3.3; Length 1220;
Matches 58; Conservative 43; Mismatches 104; Indels 50; Gaps 11;

5 LGTLLAATLAFGAMGYITGNHVSARDIDHIYVAPRPATITQLDFMPGGRPHK 64
|||
DB 32 LGSLLILAVT-----TGVIYSNKNLR--SDRLYIAQLKSSQIDQTLNLT-----YIQ 79
|||
QY 65 PYSGVAVAFRSDITNOCYOELSEERFENCTH-----RSSVFGCKYETEF--SA 114
|||
DB 80 AYLASRDALQSSLTSTVYAGNKSADNMVDSLVYQKFLSSNLFYAKYDSSFNVLNA 139
|||
QY 115 SNRLTGPPHP-----FKLTIRPNRPNDSGMFYIVRLDDTKRPIDVFAQLSVQFAN 167
|||
DB 140 TNNGTDLIPEDVLDLPLSTDTPLP--SLFTIGILDVPLNSTD-YLMSLSLPIFAN 196
|||
QY 168 TAATRLGLYSKASCRTPGLPTVQLEAVLRTESMRNMOAYVATEATTSAEATPTPTAT 227
|||
DB 197 PSIT-----LTDSRYVGYITIIIMSA-----EGLSVFNDDTALHSHITATISAV 240
|||
QY 228 SASELEAE--HETFP 240
|||
DB 241 YNSGKASGVHVEFP 255
|||

RESULT 8
US-09-738-626-5621
Sequence 5621, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5621
LENGTH: 320
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5621

Query Match
Best Local Similarity 5.0%; Score 93; DB 9; Length 320;
Matches 62; Conservative 46; Mismatches 109; Indels 84; Gaps 14;

100 SYFVGCKYETEF--TFSSANRLTGPPH-----PKLTIRPNRPNDSGMFYIVRL 146
|||
DB 56 AVFPAPEISHYMLVTF-----GLPHEIIPVAGPIPMHLMRDAGNET-----KF 102
|||
QY 147 DDTKRPIDVFAQL---SVYQFANTATRLGLYSKASCRTPGLPTVQLEA-YLRTESMRN 202
|||

Tue May 6 18:37:37 2003

us-09-993-777-7.rapb

Page 5

Db 103 KDSMPDLVQSALILRLDLYVRRAEDAMVLLGG-----NLPSIAPAMEVDVRSRL 155
QY 203 MQAVVATEATTSA-----EATPTPTVATTS-----ASELAEHFTFPMLNGVDH 248
Db 156 YHPIVKAIAATGALRAVIRQLATSPDLIVAAEEIIRATGLPKLRGPVE----- 210
QY 249 KEPTPANENSVTVRLGTWSPPLIGVVAVVSATIGLVISIVTRMCTPHRKLDVVS 308
Db 211 -----GDLSPV-----AAARALIDSGVTEVLVINKRTESLYSESESLAS 252
QY 309 ODDEERSQ--TRESKRKPMVACINKGADQDSELEVAIVNSA-----LSPDSI 360
Db 253 YDSTPGQGVNREFTAGFLAAS--NDKSTEDSVINAVAAVNAEGSEMNYIPTDKL 310
QY 361 K 361
Db 311 R 311

SEQUENCE 9
-09-753-436-1
Sequence 1, Application US/09753436
Patent No. US2001002923A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09753,436
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 30..547
US-09-753-436-1

Query Match
Best Local Similarity 23.3%; Pred. No. 2.8;
Matches 69; Conservative 36; Mismatches 80; Indels 111; Gaps 15;

QY 103 VGCKVTEYTESASNRILGPPHFKL-----TIR-----NRPDGMRYV 143
Db 98 VYCNQSGOITGSSNITVYGLPERVELAPLPMPQVGNFTLRQVBSGR--TSLTVL 154
QY 144 VLDD-----TKEPIDVFAIQLS-----VYOFANTATRGLY 175
Db 155 LKWEELSRQAVPEPEVATVLSRDDHGAFCRTLEDMQPOGLFVNTSAPQL- 213
QY 176 SKASCRTEGLPTV--OLEA--YLTREESW-----RNMQAVVA-----TEATTT 214
Db 214 -----RTPLVLPVPPRLVAPRFLEVETSWPDCTLDGLFPASBAQVLYALGDQMINATVM 268
QY 215 SAEATTPPVVATASLELA-----EHT-FPMLNGVDVDEPTPAN 255
Db 269 NNGDILTRATATRAAGBQAREIVCNTLGERREARENITVFSPLGIVALSPT-AH 327
QY 256 ENSNTVRLGTRSPPLIGVVAVVSATIGLVISIVTRMCTPHRKLDVVSOD 311
Db 328 EGSTIVT--SCMAGARVOTLDGVPAARQ-----TAQLQINATRESDD 369

RESULT 10
US-09-870-759-73
Sequence 73, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patent In version 3.1
SEQ ID NO 73
LENGTH: 365
TYPE: PRT
ORGANISM: Mus musculus
US-09-870-759-73

Query Match
Best Local Similarity 20.4%; Pred. No. 2.2;
Matches 78; Conservative 52; Mismatches 128; Indels 124; Gaps 19;

QY 50 IOLDLPMFGORPHK-----YSGTVV-----AFRSDINOCY 83
Db 15 LQSL-----AHPHOIDLNTCYAGVFEVNGRYSISPTREADLCOAFNSTLPTMQ 69
QY 84 QELS-EERFENC-----THRSSVVGCKVTE--YTFASNR 117
Db 70 MKLALSKGFETCYGFEIGNVYIRIRIPNALICANHTGVILVNTSHTDYCFNAS-- 127
QY 118 LTGPPHPEKLTIRN-PRPDGSMFVYVRLDDPK-----EPIDVAIOLSVYGF 165
Db 128 --APPEDCSTVLDLPNSFDGVPVITLTVNNDGRTYRSKQGYRTHODIDASNT-----I 179

PRIOR APPLICATION NUMBER:	60/077791
PRIOR FILING DATE:	1998-03-12
PRIOR APPLICATION NUMBER:	60/078004
PRIOR FILING DATE:	1998-03-13
PRIOR APPLICATION NUMBER:	60/078086
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078933
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/079107
PRIOR FILING DATE:	1998-03-20
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PRIOR FILING DATE:	1998-03-25
PRIOR APPLICATION NUMBER:	60/079655
PRIOR FILING DATE:	1998-03-26
PRIOR APPLICATION NUMBER:	60/079666
PRIOR FILING DATE:	1998-03-27
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PRIOR APPLICATION NUMBER:	60/079665
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079728
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PRIOR FILING DATE:	1998-03-27
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PRIOR FILING DATE:	1998-03-31
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PRIOR FILING DATE:	1998-03-31
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PRIOR FILING DATE:	1998-03-31
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PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/081070
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081043
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081071
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081195
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081203
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081222
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081955
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081838
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082565
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704
PRIOR FILING DATE:	1998-04-21

PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085697
Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2.4; Indels 117; Gaps 16;
Matches 72; Conservative 41; Mismatches 117; Gaps 16;
5 LGTL-----ALLAATLAPGAMGIVITGNHVSARIDDDHIVAPREATIGLQIF-----55
16 LGVLVAGQMLASFEITLQCEGPVCT--EESCHTEDD---LTDNAEGFVKATFSEP 70
56 -----FMGGRPKP--YSGTVAVRPSDITNOCYOEISEREENCNTHRSSVFGVK 106
71 FLHLYSYMWILQSPAKPVEEDLLY-----LRQAMOD-----WP 106
107 VRETFYSNRLNGPPHP---FKLTIRNPRNDGSMFY-----YIVR 145
107 LGVTFYFDGSGALPGCPNREPSIIV--VQKADSGHHCSGIFQSPGPIPETARVAIT 164
146 LDD-----TKEPIDVAIOL--SYQFANTATRGVYSK 177
165 VOELFPADILRAVPSAEFQNGSPMLSCOTKLPLQRSNAALRFLFKDGRIVQSGLSSE 224
178 ASCTRTGLPTVQ-----LEAYLTBESMR--NMQAYVATEATTSAATTPPYTATS 228
225 -----FOIPTASEHSGSYWCATEDNQWKSQSPLEIRYQASSSA-----APTLPN 274
229 ASELAEHPTFPMLNCGVDHYEPTPANENSNTVRLGTMSFTL 271
275 APQKSAAGTAABEAPGGLPPLPPTPSSSDPGFSSLPMDPHL 317
RESULT 12
US-09-978-697-45
Sequence 45, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivauff, Ellen
APPLICANT: Fondy, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978.697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2.4;
Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

5 LGTL-----ALLATLAPFGAMGIVITGNHVSARIDDDHIVAPREPTLOLE----- 55
16 LGVWVAGMLAASFELIOCEGPCT-ESSCHTEDD-----LIDAREAGQVAYFSEP 70
56 -----FMGQRPKP-YSGVYRFAFRSDITNOCYELSEEFENCTRRSSVYVCK 106
71 FHLIVSYDWLLOQPAKPYEGDLV-----LRQAMOD-----WP 106
107 VHEYFASNNRLTGPMPH---FKLITRNPDPDSGMY-----VYVR 145
107 LGVTFYFDGSAIDGPPNREFSIV--VQKADSHYHCSGIFSGPGGIPETASVYAIT 164
146 LDD-----TKEPIDVPAIOL--SVQOFANTAATNGLYSK 177
165 VOELFPADILRAVPSAPQAGSPMLSCQTKLPIORSAARLFEFYDGRIVOSRLSE 224
178 ASCRTFGLPTVO-----LEAYLRTESNR-NMQAYVATEATTTSABETPTPTATIS 228
225 -----FOIPTASEDHSGSYWCEATENDQWVQSPQLEIRVOGASSSA-----APETLNP 274
229 ASELAEHFTFPMLENGVDHYEPTPANENSNTVRLGTMSPTL 271
275 APOKSAAPGTAPBEAPCPPLPPTPSSEDPGFSPLGMPDPL 317

RESULT 13
US-09-978-192A-45
Sequence 45, Application US/09978192A
Patent No. US2002017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Fejtara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottfredsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC9
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
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PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070

PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
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PRIOR FILING DATE: 1998-04-08
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PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-21
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PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
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PRIOR APPLICATION NUMBER: 60/085573
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.9%; Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%; Pred. No. 2.4; Mismatches 113; Indels 117; Gaps 16;
Matches 72; Conservative 41;

OY 5 LGTL-----ALATLAPFGAMGIVITGNHVSARIDDDHIVAPREATTQQLF-----55
DB 16 LGVLWVAQMLLASFELQCEGPVCT--EESCHTEDD---LTDAREAGVQAVATFSEP 70
OY 56 -----FMGQRPKPKP-YSGTVRAVAFRSDITNOCYQELSEERFENCRTHRSSVVGCK 106
DB 71 FHLIVSYDWLILQGPAPKPFEGDLV-----LRCQAMOD-----WD 106
OY 107 VREYTFASASNRLGPPHP--FKLITRNPPNDGMEY-----VIVR 145
DB 107 LQVITFYRDSALGPPGPNREPSITY--VQKADSGHYHCSGIRSPGPIPETASVVAIT 164
OY 146 LBD-----TRKPIDVFAIQL--SVYOFANTAAATRLYSK 177
DB 165 VOELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAAARLFSFYKDKRIVQSRGLSSE 224
OY 178 ASGRTFGLPVQ-----LEAYLRTESMR-NMQAYVATEATTSAEATPTPTATNS 228
DB 225 -----FQIPFASDHSGSTWCENATEDNOVMKOSPQLEIRVQGASSA-----APPLNP 274
OY 229 ASELAEHFTFPWLENGVDHYEPTPANENSNTVRLGTMSPTL 271
DB 275 APQKSAAPGTAPPEARGPPLPPPTPSSSDPGFSSPGMDPHL 317

RESULT 14
US-09-999-832A-45
Sequence 45, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT FILING DATE: 2001-10-24
CURRENT APPLICATION NUMBER: US/09/999,832A
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366

Query Match 4.9%: Score 90.5; DB 9; Length 359;
Best Local Similarity 21.0%: Pred No. 2.4; Mismatches 113; Indels 117; Gaps 16;
Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

QY 5 LGTL---ALAAATLAFGAMGIVITGNHVSARIDDDHIVAVAPREATTOLQF-----55
DB 16 LGVLWVAQMLLAASFETLQCEGVCT-ESSCHTEDD---LTDAREAGFOVAVYFESP 70
DB 56 -----FMPOQRPKP- YSGTVARAFRSDITNOCYQELSEERFENCNHRSSVYVGCK 106
DB 71 FHLIVSYDMLLQGPAPKPVFEGLDV-----LRQAMOD-----WP 106

QY 107 VTEYFESASNRLLTGPHP---FKLITRNPNDGMY-----VIVR 145
DB 107 LTVYFTRGSGALGPRGPRREFSITV--VOKADSGHYHCSGIFQSPGPIETASVATT 164
QY 146 LDD-----TKEPIDVFAIQL---SVYQFANTATRGLYSK 177
DB 165 VOELFAPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSARLLFFSYKDGRIYQSRGLSE 224
QY 178 ASCRFTGFLTVQ-----LEAYLRTESWR-NMOAYVATEGTTTSALATTPTPTATS 228
DB 225 -----FOITJASEDSHSGSWCEATEDNCKWOSPOLETRVQGAASSA-----APPTLMP 274

QY 229 ASELEAEHFTPMLENGVDHYEPTPANENSNTVRLGTWSPTL 271
DB 275 APOKSAAPCTABEAPAGPLPPPTFSSSEDPGESSPLGMPDPL 317

Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerder, Hanspeter
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APPLICANT: Goddard, Audrey
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APPLICANT: Gurney, Austin L.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James J.
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumaw, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 4.9%; Score 90.5; DB 9; Length 359;

Best Local Similarity 21.0%; Pred. No. 2.4; Matches 72; Conservative 41; Mismatches 113; Indels 117; Gaps 16;

QY 5 LGTL---ALMATLAPGANGIYITGNHVSARIDDDHIVIAAPPETIOLQLE-----55
DB 16 LGVIMVAMOMLAAFEITQCEBPCT-EESCHTEDD---LTDAREAGFOVKAYTSEP 70
QY 56 -----EMPGORPKP-YSGTIVAVAFRSDITNOCYOELSERENGTSSSVFVGCK 106
DB 71 PHLIVSTIDWLLDGPAPKVFEBDDLY-----LKOQAMOD-----WP 106
QY 107 VTEYTESASRLTGPHP---FKLIRNPRNNSGMFY-----YIVR 145
DB 107 LTQVTFYRDSALGPPGPKREFSTIV-VQABSGHHCSGIFQSPGCIETASVVAIT 164
QY 146 LDD-----TKEPIDVFAIOL---SYQFRNTAAIRGLYXK 177
DB 165 VOELFPAPILRAVPSAEPOAGSPMTLSCQTKLPLQNSAARLFFSKIGRIVQSRGLSSE 224

Tue May 6 18:37:37 2003

us-09-993-777-7.rapb

Page 14

Oy 178 ASCRCFGCPVQ-----LEAVLPREESR-IMQAVYVTEATSTSAEATTPPYTAN 228
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 Db 225 -FQPTASEDSHSSGYCEATEDNQWVKOSPQLEIRVQCASSA-----APPLNP 274
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 Oy 229 ASELAEHEHTPPMLNVVDHDEPPRAENSNVYRGTMSPTL 271
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Search completed: May 5, 2003, 16:26:30
Job time : 20.5 secs